

749	20469119 (1497, 1498)	Novel Protein sim. GBank			UNCLASSIFIED	264604
750	20296427 (1498, 1500)	gi 1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE)				264600
751	21636169 (1501, 1502)	Novel Protein sim. GBank		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	gi 5360068 gb AA042851.1 AF15968 - (AF159689) serine/threonine kinase PKN3 [Myxococcus xanthus]		Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank			UNCLASSIFIED	264909, 264600, 264602, 264604, 264760, 264769, 264634
754	95083741 (1507, 1508)	gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)			UNCLASSIFIED	264508, 264906, 264907, 264908, 264909, 264759, 264602, 264764, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
755	80185449 (1509, 1510)	Novel Protein sim. GBank			UNCLASSIFIED	264448, 264690
756	94631686 (1511, 1512)	(AL031317) putative dehydrogenase [Streptomyces coelicolor]				264769, 264689, 264638, 264639
757	79468533 (1513, 1514)	Novel Protein sim. GBank			UNCLASSIFIED	264682, 264685
758	78963176 (1515, 1516)	(AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]			amylase	265007, 18108387, 265007, 18108387
759	78475667 (1517, 1518)	Novel Protein sim. GBank			UNCLASSIFIED	264684, 264686
760	87628888 (1519, 1520)	Novel Protein sim. GBank		Contains protein domain (PF00122) - E1-E2 ATPase	transport	29331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265018, 264681, 264687, 264688, 21906766, 21906768, 265020, 265021, 265022, 264635, 22279000
761	79877966 (1521, 1522)	Novel Protein sim. GBank			UNCLASSIFIED	264766
762	80023563 (1523, 1524)	(AB014572) KIAA0672 protein [Homo sapiens]			UNCLASSIFIED	264907, 264593, 265020
763	20294813 (1525, 1526)	Novel Protein sim. GBank				264600
764	39515024 (1527, 1528)	gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB [Thermotoga maritima]				264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gjl3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	264905, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)				
767	10296742 (1533, 1534)	Novel Protein sim. GBank gjl541121pir[S40827 - hypothetical protein o300 - Escherichia coli]		UNCLASSIFIED	264605, 264762, 18108374
768	79416080 (1535, 1536)				264907
769	80086554 (1537, 1538)	Novel Protein sim. GBank gjl2982501[emb CAA06164] - (AJ004832) neuropathy target esterase [Homo sapiens]		UNCLASSIFIED	264592, 264595
770	80417847 (1539, 1540)	Novel Protein sim. GBank gjl283437pir[S27850 - hypothetical protein - Trypanosoma cruzi (fragment)]		esterase	55810764, 264559
771	95329508 (1541, 1542)	Novel Protein sim. GBank gjl4769004[gb AAD29715.1 AF140598] ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264905, 264907, 264828, 264909, 265010, 264766, 264628, 264629, 264634, 264636, 264555
772	78971362 (1543, 1544)			UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 87168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
773	78945363 (1545, 1546)			UNCLASSIFIED	264910
774	79856129 (1547, 1548)	Novel Protein sim. GBank gjl5531324[emb CAB51045.1] - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	265020
775	20620141 (1549, 1550)			UNCLASSIFIED	264909
776	78942693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	264555
777	79960378 (1553, 1554)	Novel Protein sim. GBank gjl4505461[ref NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)]	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 264691
778	20601310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	85288987 (1559, 1560)	Novel Protein sim. GBank gjl1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				
782	8758529 (1563, 1564)	Novel Protein sim. GBank gjl4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
783	16410791 (1565, 1566)				264605
784	80051197 (1567, 1568)				265020
785	56073541 (1569, 1570)	Novel Protein sim. GBank gjl3451335 (AC005525) - F22162_1 [Homo sapiens]		UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264566
786	20438842 (1571, 1572)	Novel Protein sim. GBank gjl136748[sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 264604
787	80258364 (1573, 1574)		transport		264603
				UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gjl2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gjl2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium cutirubrum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gjl5706378 [dbj]BAA83099.1] - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21906765, 21906767, 21906768, 21906769, 265020, 264692, 22279000, 264563
791	94651627 (1581, 1582)	Novel Protein sim. GBank gjl5689948 [emb]CAB51985.1] - (AL109863) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264636
792	80058786 (1583, 1584)	Novel Protein sim. GBank gjl393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gjl1345408 [dbj]BAA05046] - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gjl105884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gjl1877334 [emb]CAB07082] - (Z92771) bfrA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264907, 265010, 35698423, 264636
796	86669451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gjl2995447 [emb]CAA71519] - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 66714117, 21906767, 21906769, 265020, 265022
798	79865209 (1595, 1596)			transcriptfactor	264687, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gjl4467250 [emb]CAB37575] - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264636, 264638
800	79970189 (1599, 1600)			UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank gjl2791517 [emb]CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	264508, 264511, 265006, 265009, 264769, 264567, 264486
802	79834598 (1603, 1604)	Novel Protein sim. GBank gjl4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264905, 264693
803	20467520 (1605, 1606)			struct	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gjl1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		kinase	264510
805	79599993 (1609, 1610)				264508
806	80484113 (1611, 1612)	Novel Protein sim. GBank gjl2764612 [emb]CAA04683] - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gjl2833311 [sp]Q21828 [YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gij3913092[sp]Q46170[ARCD_CLOPE - ARGININE/ORNITHINE ANTIporter]		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gij3913016[sp]P74309[ALF1_SYN3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)]	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gij401472[sp]P30863[YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gij146168 (J01617) - glutaminyl- (tRNA synthetase [Escherichia coli])		synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gij4589652[dbj]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264389, 264288, 264685, 21906765, 21906767, 265020, 265021, 264692, 65274620, 33657109, 264629, 18108376, 264635, 264638, 60170394, 56182323, 264564
816	19881910 (1631, 1632)				264600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gij178114[emb]CAB06254] - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
818	80938190 (1635, 1636)	Novel Protein sim. GBank gij1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gij1001352[dbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gij586814[sp]P37484[YVBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION]		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264594, 264637
823	84992299 (1645, 1646)	Novel Protein sim. GBank gij3878400[emb]CAA95828] - (Z71264) predicted using GeneFinder: Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		struct	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gij1370076[emb]CAA66887] - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669 - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312 - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336692 gb AAD17897 - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21906768, 35695917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264566, 264486
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetyl(muramyl tripeptide synthetase MurC [Helicobacillus mobilis]		UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)	Novel Protein sim. GBank gi 1870004 emb CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264603
831	87112435 (1661, 1662)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-L YASE ACTIVATING ENZYME		UNCLASSIFIED	66714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)		UNCLASSIFIED	264906
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-L YASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	264768, 263994, 21906767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35696052, 22279002, 264508, 264905, 264906, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 728867 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	35695917, 264557
837	78450450 (1673, 1674)	Novel Protein sim. GBank gi 728867 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264595
838	78184203 (1675, 1676)	Novel Protein sim. GBank gi 2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264687
839	79641125 (1677, 1678)	Novel Protein sim. GBank gi 2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gil139805 sp P08045 XFIN_XENLA - XFIN PROTEIN	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gil2114321 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gil3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gil2224721 dbj BAA20844 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	265011
845	18346844 (1689, 1690)				264629
846	79863441 (1691, 1692)	Novel Protein sim. GBank gil625679 pir A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	264907
847	78595348 (1693, 1694)				264909
848	78489365 (1695, 1696)			UNCLASSIFIED	265020
849	79756367 (1697, 1698)			UNCLASSIFIED	264568
850	79817849 (1699, 1700)	Novel Protein sim. GBank gil3183245 sp P78061 YCJL_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gil5454130 ref NP_008280.1 pTLN - talin	Contains protein domain (PF01608) - ILWEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433358, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264369, 264685, 264768, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52844150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gi 3402836 emb CAA76082 - (Y16136) 2-enoate reductase [Moorella thermoacetica]			264636
854	80052438 (1707, 1708)		reductase		264566
855	78641130 (1709, 1710)				264692
856	11594236 (1711, 1712)		UNCLASSIFIED		264591
857	79210165 (1713, 1714)		UNCLASSIFIED		264630, 264634
858	80248910 (1715, 1716)				265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)				264559
860	80041749 (1719, 1720)		UNCLASSIFIED		264489
861	65857045 (1721, 1722)		UNCLASSIFIED		33657023, 264630
862	80079467 (1723, 1724)				264600
863	80579931 (1725, 1726)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	UNCLASSIFIED		264488, 18108398, 35696286, 264259, 18108351, 264288, 265021
864	94939904 (1727, 1728)		UNCLASSIFIED		264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gi 5689884 emb CAB52047.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		Contains protein domain (PF01479) - S4 domain	264635, 264600, 284636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gi 4557876 ref NP_000341.1 pABCR - ATP binding cassette transporter	transport		264288, 264557, 264558
867	80062402 (1733, 1734)				264605
868	10075364 (1735, 1736)		UNCLASSIFIED		264909
869	80062406 (1737, 1738)				264605, 264687, 18108374
870	80249651 (1739, 1740)	Novel Protein sim. GBank gi 628660 pir S37755 - Adenylyl-transferase - Escherichia coli	transferase		264601, 264636
871	20378295 (1741, 1742)	Novel Protein sim. GBank gi 1708180 sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG	UNCLASSIFIED		264603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gi 1545959 emb CAA67763 - (X99384) paladin [Mus musculus]	UNCLASSIFIED		35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264596, 52646317, 87168474, 265010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52644229, 264769, 21906765, 265021, 264534, 264691, 52645129, 264628, 264629, 35696423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264564
873	20189728 (1745, 1746)	Novel Protein sim. GBank gi 4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	UNCLASSIFIED	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264595

874	80077692 (1747, 1748)	Novel Protein sim. GBank gi 134319 sp P07819 SCRB_BACSU - SUCROSE-8- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gi 481000 pir S37594 - mucin - human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gi 3128283 (AF010496) - iron(iii) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF00005) - ABC transporter	transport	264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi 731074 sp P40349 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - GATA zinc finger	transcriptfactor	22278998, 264908, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi 1351614 sp Q09853 YAEI - SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase_associated	264369, 264555
879	94328862 (1757, 1758)	Novel Protein sim. GBank gi 3875304 emb CAA98434 - (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609 comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...			56182575, 293331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21908768, 21908768, 80170815, 33657023, 65274620, 33657109, 18108374, 35695855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi 137120 sp P11214 UR0T_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kringle domain	cathepsin	264508
881	11290122 (1761, 1762)			UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi 2632098 emb CAA75667 - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	264558
883	79582969 (1765, 1766)			UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi 1155068 emb CAA64425 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi 2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362
886	11685136 (1771, 1772)				264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi 2695834 emb CAA15904 - (AL021006) sucA [Mycobacterium tuberculosis]		dehydrogenase	35696052, 264906, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gi 5689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED	264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi 1881338 dbj BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959398 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank 1D=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namalwa cells, Peptide, 541 aa]		transcriptfactor	22278986, 22278999, 29331828, 35696052, 264908, 264909, 265009, 265011, 264602, 265019, 264766, 21906765, 21906766, 21906769, 265020, 265021, 56526486
893	78168037 (1785, 1786)	Novel Protein sim. GBank gi 2829888 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase	264689, 263967
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)				264632
897	94991823 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264686, 29331828, 264511
898	87895109 (1795, 1796)				56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264486
899	11100463 (1797, 1798)				264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]		transport	264769, 264691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 3355701 emb CAA20001 - (AL031124) 3-Isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060206 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35696052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21906764, 35695917, 27486262, 35695855, 264634, 264636, 264486
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264909
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)			UNCLASSIFIED	60432289, 264601, 264690
908	11754482 (1815, 1816)			UNCLASSIFIED	264638
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3868940 dbj BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264602
910	16776206 (1819, 1820)	Novel Protein sim. GBank gi 4589726 dbj BAA76883.1 - (AB003137) DnaJ homolog protein [Salix gligiana]	Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)	eph	265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20469357 (1825, 1826)			UNCLASSIFIED	264604
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 dbj BAA83069.1 - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264906, 264591, 21906768, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)			UNCLASSIFIED	264605
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carter]		synthase	264259, 29331826, 264908, 265019, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689568 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79606095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1 - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78982605 (1843, 1844)				265019, 22279002
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)	Novel Protein sim. GBank gij4115936[jgb]AAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij4490609[emb]CAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij5459396[emb]CAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gij5689523[dbj]BAA83045.1] - (AB029016) KIAA1093 protein [Homo sapiens]		transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij119111[sp]P12978[EBN2_EBV - EBNA-2 NUCLEAR PROTEIN]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)				264369, 22279002
935	80063162 (1869, 1870)			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 264602, 264667, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669[pir]CGHU1V - collagen alpha 1(V) chain precursor - human		synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij2226243[emb]CAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	264602
939	11071694 (1877, 1878)				
940	94144252 (1879, 1880)	Novel Protein sim. GBank gij3560166[emb]CAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264600 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)				264593
942	19484122 (1883, 1884)			UNCLASSIFIED	264760
943	80080256 (1885, 1886)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264600, 264687, 264689, 264563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]		synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353[sp]P39606[YWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION]	Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	78248402 (1891, 1892)				265017

947	81802699 (1893, 1894)	Novel Protein sim. GBank gjl2896770 emb CAA17247 - (AL021899) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gjl2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		tgf	18108398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gjl4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27486261, 21906766, 52644296, 33657349, 87168518, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	79455872 (1899, 1900)	Novel Protein sim. GBank gjl1079461 pir S43865 - cytochrome b, type II - poliovirus (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gjl5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gjl5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		calthepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gjl2495842 sp Q47142 YFHS_ECOLI - HYPOTHETICAL 41.6 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9893326 (1907, 1908)	Novel Protein sim. GBank gjl2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gjl5454064 ref NP_006319.1 pSIP - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	55994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gjl2052129 emb CAB08155 - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056206 (1913, 1914)	Novel Protein sim. GBank gjl1709787 sp Q00451 PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gjl2131050 emb CAB09260 - (Z95844) opca [Mycobacterium tuberculosis]		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gjl2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)			UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

863	80590374 (1925, 1926)				UNCLASSIFIED	264510, 264288, 264555, 264556, 264558, 264559, 264486
864	79832019 (1927, 1928)	Novel Protein sim. GBank gij4589622[dbj BAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	264112, 264910, 264689
865	91229485 (1929, 1930)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
866	95292815 (1931, 1932)				UNCLASSIFIED	264906, 264592, 264596, 264604, 264768, 21906764, 264692, 264693, 264629, 264636, 264638
867	79255708 (1933, 1934)	Novel Protein sim. GBank gij1731207[sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	264760
868	79560269 (1935, 1936)	Novel Protein sim. GBank gij2661836[emb CAA75187] - (Y14984) putative transport protein [Methylophilus methylotrophus]			transport	264693
869	79919470 (1937, 1938)	Novel Protein sim. GBank gij5419878[emb CAB46422.1] - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		dna_ma_bind	35696286, 264685, 264686, 35695917, 264692, 18108374, 264635
870	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21908767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
871	78919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
872	20710704 (1943, 1944)					264557
873	20370183 (1945, 1946)	Novel Protein sim. GBank gij1723119[sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				264604
874	80057103 (1947, 1948)				UNCLASSIFIED	264565
875	10196018 (1949, 1950)				UNCLASSIFIED	264510
876	80205742 (1951, 1952)	Novel Protein sim. GBank gij3881459[emb CAA92988.1] - (Z68753) predicted using Genefinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...			UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
877	10355349 (1953, 1954)	Novel Protein sim. GBank gij549456[sp Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	264906
878	80025927 (1955, 1956)				UNCLASSIFIED	264600, 264602, 264603, 264604
879	80447820 (1957, 1958)	Novel Protein sim. GBank gij3171904[emb CAA75869] - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	264767, 264768, 265008, 265007, 264906
880	80025928 (1959, 1960)				UNCLASSIFIED	264600, 264602, 264605
881	80096550 (1961, 1962)	Novel Protein sim. GBank gij3599940 (AF017368) - facogental dysplasia protein 2 [Mus musculus]			UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1963, 1964)	Novel Protein sim. GBank gij2950220[emb]CAA71575] - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90895041 (1965, 1966)	Novel Protein sim. GBank gij476389[pir]B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466876 (1967, 1968)			UNCLASSIFIED	264605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gij3451504[emb]CAA07660.1] - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264909
988	19858661 (1975, 1976)			UNCLASSIFIED	264600
989	88095328 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gij5725506[gb]AAD48080.1]AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Repolysin (M12B) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264766, 264628, 264635, 264568
991	10106140 (1981, 1982)			UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[emb]CAB08835] - (Z95436) hypothetical protein Rv3645 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)				264907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gij5106572[gb]AAD39760.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 55274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 264692, 264693, 264629, 35696423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22279002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264906, 264565, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[sp]P04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506897 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	264682
1000	20727944 (1999, 2000)			UNCLASSIFIED	264602
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 dbj BAA20833 - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264907, 264909, 264511, 264603, 264683, 264684, 264687, 264689, 29148627, 21906769, 264692, 18108385, 22279000
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		struct	265009, 264369, 265020
1003	17833491 (2005, 2006)				265019
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264635
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi 4062979 dbj BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1 - (AJ001206) putative trehalase synthase [Streptomyces coelicolor]		synthase	265007, 264602, 264605, 264760, 264636
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342647 gb AAB86591.1 - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264905, 264764, 264768, 35695917, 264629
1012	95294456 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264905, 264600, 264601, 264602, 264605, 264762, 264766, 264768, 264689
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21906768
1014	86608828 (2027, 2028)				29331824, 265019, 265020

1015	95418878 (2029, 2030)	Novel Protein sim. GBank gij4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	struc	22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 264510, 264591, 264593, 60433356, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811857, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35696423, 264630, 22279000, 264565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gij2506969[sp]P41407[ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)]		esterase	264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943[dbj]BAA79259.1] - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973[emb]CAB39032.1] - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278986, 29148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264688, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807[gb]AAD26859.1[AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230[emb]CAB06277] - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264558, 18108388, 264586
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gij3483045[emb]CAA20556] - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gij1174922[sp]Q02322[UVRD_HAEIN - DNA HELICASE II [Streptomyces coelicolor]		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728[ref]NP_004886.1[pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20297828 (2055, 2056)	Novel Protein sim. GBank gij2791409[emb CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ref NP_000145.1 pGALK - galactokinase 1]		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35696052, 264908, 264510, 18108354, 264687, 264769, 264689, 80431602, 18108385, 264486
1034	78245937 (2067, 2068)	Novel Protein sim. GBank gij405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	78956355 (2069, 2070)			UNCLASSIFIED	264692
1036	85804998 (2071, 2072)				264905, 66712502, 264908, 264766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLATLH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - isomerase		264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gij3256535[dbj BAA29218.1 - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]	kinase		264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb CAA66953] - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gij1870167[emb CAA70125] - (Y08921) msik [Streptomyces reticuli]	Contains protein domain (PF00005) - transport ABC transporter		264565, 264567
1044	80025952 (2087, 2088)			UNCLASSIFIED	265006, 264602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gij5689890[emb CAB52053.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			29331825, 264637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij954065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]	helicase		264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij4210471[dbj BAA74535.1 - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij3413419[emb CAA20279] - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686

1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442962 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21906754, 52645156, 56182435, 264689, 29331827, 27486261, 35696052, 21908765, 35696423, 21906768, 56182575, 21906769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)				UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AAD38584.1 AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase		helicase	264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 dbj BAA25358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80376576 (2115, 2116)					264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gi 1170016 sp P46808 GREM_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREM (TRANSCRIPT CLEAVAGE FACTOR GREM)			transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir J28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp Q49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)			dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi 2499966 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir JJA0086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385

1065	60021208 (2129, 2130)	Novel Protein sim. GBank gi 2120998 pir S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	264600, 264602, 264689
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gi 2506362 sp P15042 DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)				264909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gi 4007669 emb CAA22335 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264888, 18108382, 264558, 264600, 264760
1069	83002854 (2137, 2138)	Novel Protein sim. GBank gi 4589484 dbj BAA76770.1 - (AB023143) KIAA0926 protein [Homo sapiens]		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gi 120304 sp P15932 FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	264604, 264760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gi 1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1072	82356540 (2143, 2144)			UNCLASSIFIED	264687, 264688, 21906784, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264905, 264690, 264906, 264762, 264628, 264768
1073	79814400 (2145, 2146)				264909
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gi 477532 pir A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264906
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gi 3893109 emb CAA76940 - (Y17820) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264369, 264688, 265020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gi 1176203 sp P48442 YHGM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)		ATPase_associated	264769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gi 4033487 sp Q44472 TUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1078	20288874 (2155, 2156)			UNCLASSIFIED	264600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gi 3413828 emb CAA20296 - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1080	11767188 (2159, 2160)			UNCLASSIFIED	264684
1081	94747080 (2161, 2162)				83373044, 265019, 22279002, 264482, 18108351, 264682, 264908, 264693, 264487
1082	81490656 (2163, 2164)			UNCLASSIFIED	264758, 264768, 264769, 21906767, 264511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gi 1722945 sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424178, 264905, 264906, 264510, 60432229, 264759, 87168474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636 264769
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gi 418384 sp P32057 WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gi 1899190 (U90204) - heat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family		60432229, 264687
1086	78608269 (2171, 2172)	Novel Protein sim. GBank gi 1172958 sp P46176 RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gi 4160198 emb CAA15431 - (AL008583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 264693
1088	78854963 (2175, 2176)	Novel Protein sim. GBank gi 2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gi 4981768 gb AAD36280.1 AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gi 4007680 emb CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gi 2495562 sp P77239 YLCQ_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252285 (2183, 2184)	Novel Protein sim. GBank gi 2960098 emb CAA17996.1 - (AL022121) nth [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264566 264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gi 1001642 dbj BAA10373 - (D64002) dGTP triphosphohydrolase [Synecocystis sp.]		UNCLASSIFIED	264686
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gi 4585587 emb CAB40855.1 - (AL049628) putative adenine glycosylase [Sireptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264766, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gi 115001 sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1097	79239560 (2193, 2194)	Novel Protein sim. GBank		UNCLASSIFIED	265019
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gi 114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	264687

1099	39523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE-N1)-METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp Q64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	- isomerase	264769
1102	79777614 (2203, 2204)			UNCLASSIFIED	264910, 264909
1103	61897259 (2205, 2206)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 29335448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21906754, 264555, 264556, 264558, 22279002
1105	80255121 (2209, 2210)				264566
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264369
1107	80470019 (2213, 2214)				264908, 264769
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338 - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	264602, 264605, 264636
1110	80503554 (2219, 2220)				264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			18108370, 264557
1112	95010088 (2223, 2224)				264908
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA19628 - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264600, 264602, 264604, 264605, 264762, 264769, 264565
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264636
1115	11765583 (2229, 2230)				
1116	79841152 (2231, 2232)			UNCLASSIFIED	264686
					264908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gi 3255965 emb CAA94089 - (Z70200) US snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 28146498, 264508, 264905, 264509, 264908, 264907, 264908, 66712502, 264909, 52844045, 56182435, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109854, 33657084, 265011, 87168559, 284600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264784, 264683, 264288, 264369, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	79563326 (2235, 2236)			UNCLASSIFIED	264691
1119	79642463 (2237, 2238)			UNCLASSIFIED	264907
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi 1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264563
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi 98800 pir S17768 - 3-dehydroquinase synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264693, 27486285
1124	79811596 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2249, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi 138154 sp P03643 VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264682
1128	8384885 (2255, 2256)	Novel Protein sim. GBank gi 5002704 emb CAB44358.1 - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)			UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gi 4981328 gb AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	35696286, 22278998, 29331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278996, 264906, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17280437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gi 4539171 emb CAB39700.1 - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	78842052 (2271, 2272)	Novel Protein sim. GBank gi 4982454 gb AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gi 4972746 gb AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22278998, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gi 731607 sp P38739 YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	struct		264908
1139	79633561 (2277, 2278)	Novel Protein sim. GBank gi 3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]	UNCLASSIFIED		264693
1140	39480358 (2279, 2280)		UNCLASSIFIED		264593
1141	79638019 (2281, 2282)		UNCLASSIFIED		265019, 264693
1142	19635848 (2283, 2284)		UNCLASSIFIED		264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gi 3928000 emb CAA05880 - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain		56182575, 264908, 264600, 264632, 87168518
1144	80088988 (2287, 2288)		UNCLASSIFIED		264635, 264636, 264907, 264593, 264908, 264566, 264909
1145	14610262 (2289, 2290)		UNCLASSIFIED		264112
1146	82062092 (2291, 2292)		UNCLASSIFIED		264769, 264689, 35696286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gi 2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1 - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]			ATPase-associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264598, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655[gbjAAD16978] - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]			polymerase	264595
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275[embjCAB07311.1] - (Z92825) predicted using Genefinder; Similarity to Yeast low affinity glucosa transporter HXT4 (PS:32467); cDNA EST EMBL:C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...			glycoprotein	264488, 22278988, 264905, 264629, 264486
1153	80027783 (2305, 2306)					
1154	83002995 (2307, 2308)	Novel Protein sim. GBank gij4240315[dbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	264910, 264555, 264557
1155	79411098 (2309, 2310)				UNCLASSIFIED	264690, 264636
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij586655[spP37617/ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZNI)-TRANSLATING P-TYPE ATPASE]		Contains protein domain (PF00122) - E1-E2 ATPase	transport	264603
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij418480[spP32139/YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION]			UNCLASSIFIED	264906, 264907, 264758, 264766, 264769, 264689, 264638, 264566
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij2496481[spIQ50724/YO9S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C]				264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79186451 (2317, 2318)					264687
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gij1136406[dbjBAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]				29331822, 29331824, 66714117, 29331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563
1161	7417143 (2321, 2322)					264369
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij2443342[dbjBAA22380] - (D88764) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	264693
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij4503375[refINP_001376.1]pDPYS - dihydropyrimidinase			UNCLASSIFIED	29331827, 264906
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij5052554[gbjAAD38607.1]AF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			transport	18108398, 29331827, 29331828, 29146498, 29146499, 18108354, 21906768, 29148627, 21906769, 264693, 18108382, 18108385
1165	80491888 (2329, 2330)				UNCLASSIFIED	264602, 264605, 264769, 18108370, 18108374, 264565
1166	88096456 (2331, 2332)	Novel Protein sim. GBank gij4589476[dbjBAA76766.1] - (AB023139) KIAA0922 protein [Homo sapiens]				264488, 35696286, 22278999, 264259, 66714117, 60432289, 35696052, 264905, 56182435, 265006, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113

1167	78963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		Kinase	264488
1168	88094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264568
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772914 (AF029249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757846[ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35696052, 264634, 264486
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[dbj BAA22946] - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264909, 264591, 264632, 264638, 264639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb CAA17520] - (AL021958) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij118333[sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264905, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij119791[sp P28643 FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	65274572, 18108398, 22278998, 22278999, 29331826, 264508, 264908, 264828, 33657402, 33109954, 264769, 21906765, 21906768, 21908768, 55811957, 33657023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2960090[emb CAA17988.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb CAA04787] - (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17846362 (2361, 2362)			UNCLASSIFIED	265017
1182	81484284 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			265007, 265009, 264564, 264909, 264693
1183	78574044 (2365, 2366)				264689, 35696423, 264638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]		UNCLASSIFIED	264602
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gij2129478[pir S51839 - chitinase (EC 3.2.1.14) precursor - beet		glycoprotein	263967

1186	20224012 (2371, 2372)			UNCLASSIFIED	264559	
1187	79248834 (2373, 2374)			UNCLASSIFIED	29331825, 265017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synechococcus PCC7002]		UNCLASSIFIED	264905, 264906	
1189	79609367 (2377, 2378)				264692	
1190	78930589 (2379, 2380)			UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)			UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486	
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRFamide related peptide family		264636	
1193	11103584 (2385, 2386)			UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1790277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	264605	
1196	13000688 (2391, 2392)				264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2497360 sp Q50715 IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain	dehydrogenase	264594	
1198	95280101 (2395, 2396)				264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1709525 sp P54673 P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)			264259, 264757, 33109954, 21906768	
1200	9848880 (2399, 2400)			UNCLASSIFIED	264910	
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 2499877 sp P70645 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)		cathepsin	264766, 264769	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]		ribosomalprot	264600, 264558	
1203	82125373 (2405, 2406)			UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909, 264766	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT			264905, 264769, 264636	
1205	80053981 (2409, 2410)			UNCLASSIFIED	264566	
1206	80241865 (2411, 2412)			UNCLASSIFIED	264556, 264557, 264558	
1207	79841192 (2413, 2414)				29331824, 264909, 265021, 18108370	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gil1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	58426884 (2419, 2420)			UNCLASSIFIED	264907, 264693
1211	94656555 (2421, 2422)	Novel Protein sim. GBank hypothetical protein o246 - Escherichia coli		transferase	264591, 264592, 264595
1212	79167929 (2423, 2424)	Novel Protein sim. GBank gil3880625 emb CAB07858 - (Z93785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gil226292 pir J1505375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gil5726285 gb AA048396.1 AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050106 (2429, 2430)	Novel Protein sim. GBank gil3226739 emb CAB10953 - (Z98268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gil417329 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gil1805460 dbj BAA09022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264601
1219	91216252 (2437, 2438)				56181686, 29331822, 60432289, 264601, 264692, 264629
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gil4240315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52844507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gil2143886 pir J152523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gil730805 sp P39663 SPHR_SYNTP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gil1172627 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gi 2105050 emb CAB08836 - (Z95436) hypothetical protein Rv3544c [Mycobacterium tuberculosis]			264768
1226	80237518 (2451, 2452)			polymerase	264905, 264512, 264689
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gi 1706768 sp P98133 FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)		UNCLASSIFIED	264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gi 1653901 db BAA18811 - (D90917) acriflavine resistance protein [Synechocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		264605, 264634
1229	94329135 (2457, 2458)			UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gi 116230 sp P28598 CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	264909, 264605, 18108388
1231	79843141 (2461, 2462)			UNCLASSIFIED	264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gi 1215733 (U48718) - OphC [Agrobacterium tumefaciens]		transport	264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gi 116298 sp P20730 CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)		UNCLASSIFIED	265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gi 1729671 sp P40280 H2A_MAIZE - HISTONE H2A	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4	histone	265008, 265010, 18108381
1235	79814423 (2469, 2470)				264634, 264762
1236	81927147 (2471, 2472)			UNCLASSIFIED	265018, 5581150, 264565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gi 3875133 emb CAA94750 - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL...			264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gi 3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 29331824, 35696052, 264508, 264908, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gi 4007990 gb AAC95339 - (AF084363) DOK protein [Mus musculus]		oncogene	264509, 264511, 264759, 264760, 264764, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gi 1176192 sp P45420 YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gi 121383 sp P18904 GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264601, 264604, 264638
1242	79775890 (2483, 2484)				264906, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gi 335567 emb CAA19971 - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gi 2970846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gi 4586338 dbj BAA76357.1 - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gi 3581849 emb CAA20805 - (AL031541) putative phenylalanine-HRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gi 2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gi 1352403 sp P09467 F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 29331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gi 2791407 emb CAA16001 - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gi 112785 sp P05100 3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gi 5670176 gb AAD46616.1 AF16131 - (AF161317) NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gi 103160 pir S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906767, 55811957, 264692, 264556, 264639
1255	79169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gi 2995353 emb CAA04608.1 - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gi 3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084606 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gij5689511[kbj]BAA83039.1] - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264908, 264768, 264769, 264689, 264693, 264639, 18108384, 264563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gij95100[pir][S21334 - hypothetical protein 4 - Agrobacterium tumefaciens]		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)				264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gij3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264634
1265	80253578 (2529, 2530)				264563
1266	79914604 (2531, 2532)			UNCLASSIFIED	264766, 264636, 264638, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gij1085002[pir][S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21906754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gij4886445[emb][CAB43370.1] - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18103398, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906767, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22278002, 264486
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gij3334791[emb][CAA19939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gij2851634[sp][Q50591][Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01]	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gij1655665[emb][CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)				
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gij123726[sp][P10413][HTPG ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C62.5)]	Contains protein domain (PF00183) - Hsp90 protein	UNCLASSIFIED - eph	264905, 264908, 264909, 264769
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gij2129478[pir][S51939 - chitinase (EC 3.2.1.14) precursor - beet]		UNCLASSIFIED	264369
1277	20438195 (2553, 2554)				
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gij1175473[sp][P44555][YAAJ_HAEIN - HYPOTHETICAL PROTEIN HI0183]		UNCLASSIFIED	264556
				UNCLASSIFIED	264603
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gij1929513 (U64318) - ATP synthase subunit beta [Moorella thermoacetica]		synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gij4938504[emb][CAB43862.1] - (AL078465) putative protein [Arabidopsis thaliana]		struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gij1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gij3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gij3261721[embjCAB07057] - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gij3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gij417154[spjP33126]HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - eph		264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gij2078004[embjCAB08451] - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264638, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gij5353510[gbjAAD42161.1]AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264288, 264685, 264766, 264687, 264768, 264769, 265020, 265021, 264534, 264692, 18108370, 264628, 18108374, 35696423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391
1289	11813647 (2577, 2578)			UNCLASSIFIED	264637
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gij1169995[spjP46023]GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gij2072674[embjCAB08305] - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gij1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	264092, 264259, 29331822, 29331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265019, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 264563
1293	80067536 (2585, 2586)			UNCLASSIFIED	265006, 55812038, 264369, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gij2129173[pirj]F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		biotindep	264602, 264605, 264760, 18108351, 264689, 33657023, 264559
1295	11686851 (2589, 2590)	Novel Protein sim. GBank gij5441779[embjCAB46803.1] - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	dehydrogenase		264689

1296	11687804 (2591, 2592)	Novel Protein sim. GBank				264591, 264639
1297	78639300 (2593, 2594)	gi 4982191 gb AAD3686.1 AE00180 - (AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	polymerase	264693
1298	94239508 (2595, 2596)	Novel Protein sim. GBank gi 1943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]		struct		18108348, 265017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31665.2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor		264488, 264906, 264909, 22278002, 264566
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 4062973 dbj BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED		264605
1301	17839614 (2601, 2602)					264906
1302	95416188 (2603, 2604)					85658542, 265020
1303	8684121 (2605, 2606)					264908
1304	78377196 (2607, 2608)			UNCLASSIFIED		264508
1305	19905899 (2609, 2610)					264566
1308	13069230 (2611, 2612)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED		264636
1307	82201028 (2613, 2614)	Novel Protein sim. GBank gi 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	reductase	264907, 264992, 264764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi 95819 pir S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport		264906, 18108354
1309	78263011 (2617, 2618)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED		264605
1310	20466319 (2619, 2620)					
1311	87613142 (2621, 2622)					35696286, 293331827, 264908, 265008, 264764, 264766, 264686, 21906767, 21906769, 35695917, 264691, 264693
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi 4455118 gb AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind		22278995, 22278996, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22279002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot		22278996, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1314	56926053 (2627, 2628)					264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi 2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept		264691

1316	85361609 (2631, 2632)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 29331822, 29331824, 60424268, 29331825, 35696052, 52644045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 264584
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gi 4836757 gb AAD30541.1 AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 284808, 264808, 264369, 264884
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gi 4680204 gb AAD27567.1 AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108368, 264628, 284629, 18108377, 284638
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gi 4240183 dbj BAA74870.1 - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gi 4886505 emb CAB43377.1 - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gi 5262591 emb CAB45736.1 - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906768, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264758, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264563, 284584, 264585, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gi 3294501 (U64857) - similar to the DPT/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gi 1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322887 (2653, 2654)	Novel Protein sim. GBank gil728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 284091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264885, 264768, 264688, 21906767, 21906769, 29148629, 265020, 264690, 264691, 264692, 264693, 263967, 33657109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 35895855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 284482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gil4678224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gil437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56526486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gil4589586 dbj BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gil5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 58182435, 264510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gil5689527 dbj BAA83047.1 - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gil2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gil4240285 dbj BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 284288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486264, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi465445[sp]P33485[VNUA_Prvka - PROBABLE NUCLEAR ANTIGEN				264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi5689471[dbj]BAA83019.1] - (AB028990) KIAA1067 protein [Homo sapiens]			UNCLASSIFIED	56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432289, 29331826, 264908, 264908, 264909, 264112, 265008, 265009, 60433358, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21806766, 21906769, 265020, 264691, 27486281, 20281069, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264587
1338	80366114 (2675, 2676)				UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]			UNCLASSIFIED	35698052, 264909, 264688, 264556, 264558
1340	88316311 (2679, 2680)					264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)					264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi5019564[emb]CAB44507.1] - (AL035542) dJ984E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - tm7 7 transmembrane receptor (rhodopsin family)			264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543[ref]NP_001384.1[pecm2 - extracellular matrix protein 2	Contains protein domain (PF00560) - struct Leucine Rich Repeat			264910, 264686, 264534
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gi2144101[pir]J55210 - tricarboxylate carrier - rat (fragment)			glycoprotein	263978 264909, 60170394
1345	91225546 (2689, 2690)					
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi3881052[emb]CAA19523] - (AL023843) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain			22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264558
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379[ref]NP_003658.1[phg38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat			264806, 264908, 264908, 265008, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264567, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3399720[dbj]BAA32100] - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]			UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101[pir 55210 - tricarboxylate carrier - rat (fragment)]		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264258, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264768, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264804, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gij4887239[gb AAD32246.1] - (AF064584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101[pir 55210 - tricarboxylate carrier - rat (fragment)]			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264829, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4689108[gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21906754, 265011, 87168559, 264684, 264369, 264769, 264689, 21906765, 21906768, 52844150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij1469199[dbj BAA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21906754, 265010, 264769, 264689, 21906765, 21906768, 21906769, 264532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	95313991 (2711, 2712)	Novel Protein sim. GBank gij1113865 (U40342) - ninein [Mus musculus]		struct	18108397, 22278995, 22278996, 22278998, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264589, 21906765, 265022, 18108364, 35696423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gij97693[embjCAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87168559, 265018, 264448, 264288, 21906765, 21908768, 21908768, 265021, 264693, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gij556219 (L36831) - transcription regulator [Mus musculus]			264757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264488, 264567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gij2588282[embjCAA75612] - (Y15417) acetate--CoA ligase [Coprinus cinereus]		synthase	60432289, 264605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gij5689443[dbjBAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 264259, 29331826, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264883, 264288, 264766, 264769, 264689, 21906768, 265020, 265021, 33657023, 55811576, 35696423, 264634, 60432113, 22279002, 264482, 264488
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gij5689411[dbjBAA82989.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	- eph	56182575, 56181688, 60432049, 264259, 29331822, 56182181, 29331827, 35696052, 29331828, 264905, 264906, 264908, 264595, 55812038, 85658542, 55811150, 264681, 264288, 264369, 56181562, 60431528, 55810764, 35696423, 60431850, 264558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gij1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	264488, 29331826, 264907, 264687, 264689, 264593
1364	88179488 (2727, 2728)				60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21906766, 35696423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gij4589562[dbjBAA76803.1] - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	264766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gij1084944[pirjIS54495] - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gi 4884088 emb CAB43240.1 - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52646842, 52646365, 22278995, 56994075, 35696286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264905, 264907, 264908, 264909, 284510, 285006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21906754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264688, 264767, 264688, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gi 484561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264805, 264906, 264908, 264909, 284510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 284760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 284631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264568, 264486, 264567, 265008, 60432229, 60433356, 33657084, 21906764, 21906769, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gi 2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gi 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264768, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264638, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264566, 264488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gi 5032203 ref NP_005714.1 pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gijl840708[jdbij BAA09334] - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	263978
1373	80499421 (2745, 2746)			UNCLASSIFIED	264769, 21806765, 21806767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gijl11876[pitj JC1241 - beta-interferon-induced protein - rat		interferon	284907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1375	94236942 (2749, 2750)	Novel Protein sim. GBank gijl5648176[jgb AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 52645158, 52846842, 52646365, 56182575, 56181686, 22278998, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 60432229, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264906, 264907, 264908, 29331830, 264909, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52844296, 87188474, 87188559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810764, 35696423, 35695855, 264630, 264631, 264634, 264638, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264563, 264564, 264566, 264567
1376	87398050 (2751, 2752)	Novel Protein sim. GBank gijl138350[sp P28968 VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED	264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 58526486, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264486, 264768
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gijl1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22278002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[dbj BAA36293] - (AB001772) PEM-5 [Clona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108366, 33657109, 18108368, 264635, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb AAD30662.1] - (AF096834) germ cell specific Y-box binding protein [Homo sapiens]	nucd_rept		264510, 264512, 265008, 264288, 264564
1381	88179656 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87168559, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family		22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85658542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)		UNCLASSIFIED		18108396, 264692
1384	86915895 (2767, 2768)		UNCLASSIFIED		264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264768, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264564, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432289, 29331828, 264905, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264566
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895164[gb AAD32753.1 AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]	glycoprotein		65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35895855, 264558, 60170394, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gi 5689387 dbj BAA82977.1 - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264908, 66712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gi 3702295 (AC005783) - R33083_1 [Homo sapiens]		peptidase	52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264808, 52844045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181582, 52844229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486281, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gi 1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gi 726286 (U22394) - mSin3A [Mus musculus]			52645842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52844332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gi 2274845 dbj BAA21534 - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381

1396	95363253 (2791, 2792)	Novel Protein sim. GBank gi 2135904 pir I54810 - pHL EIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264692, 264693, 35696423
1397	87631317 (2793, 2794)			UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			264768, 18108370, 264555, 264557
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906766, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264768, 21906769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nei homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain		264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264906, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264567
1405	87612369 (2811, 2812)	Novel Protein sim. GBank gi 624076 gb AAC98425.1 - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedictum bursaria Chlorella virus 1]	collagen		264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi 2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21906765, 21906769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21906767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gi 2662165 db BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi 2493790 sp Q60994 ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 284566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gij3123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 284907, 265017, 265019, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486264, 264628, 263972, 264634, 284558, 18108385 264757
1412	84390919 (2823, 2824)	Novel Protein sim. GBank gij387912 emb CAA94370 - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED - homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52644045, 264510, 52644296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263967, 27486264, 35695763, 264639, 18108387, 264566
1413	95416559 (2825, 2826)				
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21906754, 55811386, 265017, 265018, 265019, 264761, 264683, 264369, 264288, 264686, 264689, 21906766, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486262, 27486264, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gil5106557 gb AAD39749.1 AF12305 - (AF123052) MLL seplin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29148498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21908768, 55811957, 29148629, 285020, 52644150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gil4958935 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 264908, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gil2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gil5174421 ref NP_006023.1 PCPNE - copine VI (neuronal)	ATPase_associated	28331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gil3876090 emb CAA93459.1 - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gij4505939[re]NP_000928.1pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)			56894075, 35696286, 87168559, 55811857, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gij437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264786, 264887, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gij100798[pir]S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gij2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gij5816074[gbl]AAD45616.1JAF06194 - (AF061943) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264584
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gij138350[sp]P28968[VLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264886, 65274620, 264629, 65274791, 22279002, 264566
1429	87886689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gij1181619[dbj]BAA11565] - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gij5420389[emb]CAB4680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gij414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	84708213 (2869, 2870)	Novel Protein sim. GBank gij3970850[dbj BAA34789.1] - (AB015330) HRIHFB2007 (Homo sapiens)		transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906787, 21906768, 21906769, 285020, 285021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gij3183977[emb CAA39515] - (X56044) protein Hf9C [Mus musculus]		UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gij2496887[sp Q09232]YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gij1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - kinase PDZ domain (Also known as DHR or GLGF).		264488, 264508, 264906, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264690, 35696423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gij3876299[emb CAA94892] - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...	Contains protein domain (PF00450) - cathepsin Serine carboxypeptidase		264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264636, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gij2662165[dbj BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 264259, 264908, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gij493956[emb CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....	Contains protein domain (PF00646) - F-box domain.	helicase	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264688, 21908765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gij5103027[db BAA78765.1] - (AB023419) mSox7 [Mus musculus]		transcriptfactor	264906, 265007, 264693, 264558
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gij4887229[gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447[emb CAB02772] - (Z81039) predicted using Genefinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com....		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gij2959886[emb CAA11022] - (AJ222968) L-periaxin [Mus musculus]		UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gij5081610[gb AAD39464.1 AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain		264369
1447	86945392 (2893, 2894)				18108398, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain		29331827, 264509, 264909, 265008, 264595, 18108357, 18108385, 264566, 264486

1449	87860859 (2897, 2898)				UNCLASSIFIED	66714117, 264906, 264908, 264591, 264601, 264764, 264632
1450	87458696 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35696286, 35696052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35696423, 35695855, 56528486
1451	87797970 (2901, 2902)	Novel Protein sim. GBank gij4160304[emb]CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692899 (2903, 2904)	Novel Protein sim. GBank gij2832906[dbj]BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII			kinase	264510, 264768
1454	11204696 (2907, 2908)					264556
1455	87797896 (2909, 2910)				UNCLASSIFIED	29331822, 66714117, 29331825, 264905, 29331830, 265006, 265008, 265009, 265011, 265019, 18108351, 21906768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3			transport	22278995, 22278998, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906765, 21906766, 21906767, 21906769, 29148629, 18108370, 22279000
1457	80076900 (2913, 2914)				UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264566
1459	95360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[gb]AAD44333.1[AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain		kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate			22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264760, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27486261, 264555, 83373044
1462	87732018 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gij1770466[emb]CAA66912] - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - struct 'chromo' (CHR)romatin Organization MOdifier) domain			60432049, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108385, 18108388

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gij3874447[embjCAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21906754, 265017, 265018, 264882, 264884, 264369, 264288, 264766, 21908765, 21906768, 21906767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425192 (2928, 2930)	Novel Protein sim. GBank gij4589598[dbjBAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264258, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)			UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gij4507241[refNP_003137.1]pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gij1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1470	84990482 (2939, 2940)	Novel Protein sim. GBank gij5649170[gbjAAD43131.2]AF15909 - (AF159092) syld709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21806789, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gij3876146[embjCAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL: T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13296 - (AF132968) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis- specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35696052, 264908, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21908769, 55811957, 265021, 264691, 264693, 264629, 55811576, 264634, 264638, 56182323, 22279002, 264566, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 35695917, 35696286, 264692, 33557023, 264693, 33657109, 35696052, 264508, 264905, 264908, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264486, 264685, 264766 264681, 264682, 264288, 264566
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004664.1 pANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264885, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2955, 2956)				264686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF152961) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33109954, 21906754, 265017, 265019, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657108, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 284091, 264259, 35696052, 29148499, 284103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264596, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2961, 2962)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2969, 2970)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gij4589516[dbj BAA76780.1] - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gij5019275[embj CAB44431.1] - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	21906754, 264486
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gij5712131[gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	lgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gij2497303[sp Q62786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35696423, 35895855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526486, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit ACA40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gij1656005 (U71205) - rit [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gij5689515[dbj BAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52844045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 284682, 264685, 264686, 52644229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52844332, 56182323, 87168518, 22278002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728832[sp P39189]ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 284486
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij4589588[dbj BAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	22278997, 264259, 264906, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264908, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3874925[emb CAA92591] - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene....	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526488
1498	90934938 (2995, 2996)	Novel Protein sim. GBank gij728836[sp P39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gij2570198 (U54556) - microfilarial sheath protein SHP3 [Litomosoides sigmodontis]		glucoamylase	263978, 264568
1500	80499386 (2999, 3000)			UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]		UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264558, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) [Homo sapiens]	Contains protein domain (PF00535) - transferase (Glycosyl transferases	transferase	29331822, 265007, 264369

1504	78640051 (3007, 3008)			Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102672 (3009, 3010)	Novel Protein sim. GBank gi 4753775 emb CAB41970.1 - (AJ132545) protein kinase [Homo sapiens]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264568
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gi 1304201 dbj BAA06170 - (D29768) alternatively spliced product [Rattus norvegicus]		Contains protein domain (PF00018) - SH3 domain	glycoprotein	55274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264108, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52644150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565, 264639
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gi 56889513 dbj BAA83040.1 - (AB029011) KIAA1088 protein [Homo sapiens]			helicase	
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gi 5031975 ref NP_005875.1 pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gi 113161 sp P28614 ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1510	85362643 (3019, 3020)	Novel Protein sim. GBank gi 113161 sp P28614 ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII			UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]		Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265006, 60433356, 60433438, 21908754, 87168474, 87168559, 265018, 264762, 264783, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gi 1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]				35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35696286, 56994075, 264259, 52645080, 29331822, 29331825, 35696052, 29331830, 52644045, 56182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 264448, 52644228, 21906765, 21906768, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3028, 3030)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 498015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 56182323, 22279002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 728838 sp P39195 ALU8_HUMAN - !!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!	tm7		66714117, 284508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264768, 264769, 18108374, 264636, 264638, 264486
1519	94328889 (3037, 3038)	Novel Protein sim. GBank gi 5262681 emb CAB45771.1 - (AL080198) hypothetical protein [Homo sapiens]			264569, 264489, 60432049, 265009, 33657402, 264596, 21906754, 265019, 264369, 21908765, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22279002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108364, 35696423, 264557, 264558, 18108388
1522	78950687 (3043, 3044)			UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gi 3776567 (AC005388) - Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	65274572, 21906768, 264693
1524	80203723 (3047, 3048)				
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 pRIN1 - ras inhibitor		UNCLASSIFIED	264112, 21906754, 263974
				UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gij728850]sp[P08640]JAMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gij2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264286, 21906766, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gij4406663]gb[AAD20053] - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52844045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264583, 264584, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gij2828710 (AF043642) - malrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gij1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gij3874716[embjCAA91265] - (Z66494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689	
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gij1490324[embjCAB01543] - (Z78141) unknown [Mus musculus]			sinud	29331824, 29146489, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264566	
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gij81286[pirjIS22697 - extensin - Volvox carteri (fragment)]			UNCLASSIFIED	264905, 264907, 264766, 264637	
1535	90936732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146489, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21906768, 29148629, 265021, 265022, 18108377, 56182323, 60432113, 22279000, 22279002	
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gij106024[pirjB32891 - finger protein 2, placental - human]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcriptfactor	264686, 18108357, 18108394, 21906767, 21906768, 29148629, 35696286, 265020, 265021, 52644150, 264693, 66714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35698423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766	
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gij3876332[embjCAB02096] - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113	
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gij403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388	

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gjl3218411[embjCAA19575.1] - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease ga mma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E(0.6.4e-2...		nuclease	22278994, 22278986, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 285017, 265018, 265019, 18108351, 264288, 52644229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22279000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gjl5052634[gblAAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gjl5052349[gblAAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264584, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gjl5305702[gblAAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264636, 18108381, 18108382, 264106, 33109954, 265019, 264683, 35695917, 264690, 264692, 33657109
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gjl728832[sp P39189 ALU2_HUMAN - ! ALU SUBFAMILY SB WARNING ENTRY !		nuclease	
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gjl3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nud_recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gjl1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86999594 (3093, 3094)	Novel Protein sim. GBank gjl2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3096)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168558, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264568
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gi 544483 sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264881, 264764, 264766, 264888, 264769, 21906769, 264692, 35695763, 264635, 264555, 264558, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264686, 33657109, 264558
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1 - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gjl2257495[dbj BAA21392] - (AB004534) pl015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331826, 35696052, 264508, 264905, 284908, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1556	91229268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011, 60432289, 264509, 264906, 264907, 284908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264584, 284486, 22278994, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22278000, 22279002
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gjl3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zlf-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gjl5380105[gb AAD42871.1 AF155105] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gjl112908[sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gjl3880146[emb CAA92704] - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1561	86609159 (3121, 3122)				264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1562	83359682 (3123, 3124)			UNCLASSIFIED	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1563	85508694 (3125, 3126)			UNCLASSIFIED	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gjl1168287[sp P45953 ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	264259, 29331822, 60432289, 35696052, 264508, 284907, 284908, 52644045, 264909, 284910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gij129726[sp]P05307[PDI_BOVIN] - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445[emb]CAA20329] - (AL031266) VM106R.1 [Caenorhabditis elegans]		Inf	22278996, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 66712502, 264908, 265008, 18108351, 52644228, 21906765, 21906767, 21906768, 21906769, 33657109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gij4929699[gb]AAD34110.1[AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gij4827063[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-49)]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264693, 22279000, 22279002
1569	80936668 (3137, 3138)	Novel Protein sim. GBank gij5689451[dbj]BAA83009.1] - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21908765, 21906769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86843981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF00091) - Tubulin/FtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201664 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207066 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gil4758334[ref]NP_004256.1pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 284882, 264763, 264764, 18108354, 264369, 264288, 264685, 264768, 264688, 264768, 264688, 21906765, 21906768, 21906767, 21906768, 21906769, 29148629, 264690, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22278002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gil3881810[emb]CAA94856] - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL: C08700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265006, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gil2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 63373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gil2499130[sp]P70315[WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gil2978255[jdb]BAA25190] - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35698286, 264908, 264909, 60433438, 55811388, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gil4324682[jdb]AAD16986] - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gil2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb]CAB51351.1] - (AL050306) dJ47587.2 (novel protein) [Homo sapiens]	UNCLASSIFIED		60170831, 33657402, 264682, 21806766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gb]AAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35698286, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22279002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[dbj]BAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Onchocerca volvulus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir]S52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21908769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir]I48746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	55274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27488265, 264639, 18108385, 56526486, 60432113

1590	95319825 (3179, 3180)				UNCLASSIFIED	264489, 22278996, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 52644229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 56526486, 60432113, 22279000, 22279002, 264584
1591	86877160 (3181, 3182)					
1592	87882533 (3183, 3184)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator			MHC	264259, 264905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 87168518
1593	94891661 (3185, 3186)				UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35696423, 22279000, 264565, 264567
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]			UNCLASSIFIED	264488, 29331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264602, 264604, 264760, 264681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 264628, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264584, 264566
1595	78919425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]		Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	29331826, 264908, 55811957
1596	78933928 (3191, 3192)				UNCLASSIFIED	29146498, 264758, 263967
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]		Contains protein domain (PF00067) - Cytochrome P450	UNCLASSIFIED - cyto450	264092, 29331824, 264508, 264682, 264369, 264686, 264630, 264563
1598	87862939 (3195, 3196)					264259, 264634
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)		Contains protein domain (PF01581) - FMRamide related peptide family	UNCLASSIFIED	52645080, 29331824, 29331828, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)					29331826, 264603, 264691, 264563
1601	15023246 (3201, 3202)					264635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]		Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED - struct	29146499, 264112, 264762, 18108351, 29148627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27839 - tensin - chicken			collagen	264490, 29331824, 264907, 264909, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD29633.1 AF11682 - (AF116827) unknown [Homo sapiens]			ATPase_associated	263977

1605	91221129 (3209, 3210)				struct	264905, 264509, 264906, 264907, 264908, 264909, 264604, 264766, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gij4505313[ref]NP_003794.1[p]PP - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	- struct		22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gij5174473[ref]NP_005888.1[p]PP - Intracisternal A particle-promoted polypeptide		transcriptfactor		264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gij2224629[dbj]BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED		264094, 264906, 264907, 264908, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gij4884073[emb]CAB43213.1 - (AL049934) hypothetical protein [Homo sapiens]				52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 264508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gij283920[pir]S27939 - tensin - chicken		UNCLASSIFIED		264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gij107284[pir]A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	- peroxidase		35696288, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gij3874846[emb]CAA94337 - (Z70307) Similarity to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C08951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED		264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED		264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi 4680673 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264566
1615	86121809 (3228, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265018, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3876260 emb CAB01696 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...		UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33656970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34679 YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486264
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	264684

1621	87076708 (3241, 3242)	Novel Protein sim. GBank gi 38222553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264910
1622	94741739 (3243, 3244)			UNCLASSIFIED	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29148498, 29146489, 264905, 264908, 264909, 264828, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264369, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22278002, 264566
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV122		ribosomalprot	18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35695917, 264691, 87168518, 264583
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gi 3875666 emb CAB05478 (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	66714117, 29331825, 264909, 265008, 264758
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi 4589622 dbj BAA76833.1 (AB023206) KIAA0989 protein [Homo sapiens]		kinase	264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gi 5679070 gb AAD46844.1 AF160904 (BcDNA.HL05936 [Drosophila melanogaster])			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264369, 264288, 264766, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83368773 (3253, 3254)			UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph	264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gi 4240175 dbj BAA74866.1 - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87778027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi 1915892 emb CAA69995 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264563, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi 2558501 dbj BAA22896 - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264691, 264692, 29148499, 264508, 264905, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				264488, 264259, 264807, 264808, 264909, 264628, 264629, 264631
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	265007, 264637, 22279002
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21906765, 21906768, 265021, 264690, 264482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gi 455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED - kinase	22278995, 264594, 264763, 265020, 264558
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gi 3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278996, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264829, 265007, 33657402, 21906754, 264602, 284604, 264764, 264683, 264566, 264288
1638	87101854 (3275, 3276)				264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265006, 265008, 264757, 284758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87168518
1639	94322184 (3277, 3278)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gi 2842469 emb CAA16847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gi 1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278999, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	95362691 (3291, 3292)	Novel Protein sim. GBank gi 1076802 pir S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486281, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gi 5002573 emb CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264369, 21906768, 60170615, 264639, 22279000
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1649	95347628 (3297, 3288)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264809, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264883, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108378, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487
1650	87418539 (3289, 3300)	Novel Protein sim. GBank gi 3647335 emb CAA21059 - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			265011, 264602, 21906767, 18108374, 18108377, 18108385
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906768, 21906768, 21906769, 265022, 264892, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gi 1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - struct PH domain		22278997, 29146498, 56182435, 21906754, 264369, 21906765, 21906768, 21908789, 265020, 52644150, 33657109, 22279000, 22279002
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gi 3776054 emb CAA06273 - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - glycoprotein Immunoglobulin domain		18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274791, 18108384, 60432113, 264567
1654	79756471 (3307, 3308)			UNCLASSIFIED	33657109, 264565

1655	86689346 (3308, 3310)	Novel Protein sim. GBank gi 3355717 emb CAA73496 - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526488, 60432113
1656	78962297 (3311, 3312)	Novel Protein sim. GBank gi 1890141 dbj BAA18947 - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gi 4557645 ref NP_001524.1 pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gi 2497012 sp Q10010 YSV4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331826, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52844045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264766, 264768, 264769, 21908768, 21906769, 265020, 33657023, 33657109, 65274791, 87188518, 264482, 264563, 264564, 264565, 264587
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PF27			18108392, 29331822, 29331828, 20281100, 264106, 265006, 265007, 265008, 18108348, 21908766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase WW domain		52545156, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22279000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 db BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35695917, 265021, 264534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35695855, 264634, 264635, 264555, 264638, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486

1665	91226952 (3329, 3330)	Novel Protein sim. GBank gj1083506[pil][S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain		264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gj3913431[sp]O42643DDX8_SCHPO - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00576) - S1 RNA binding domain	helicase	56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21906767, 21906769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91226655 (3333, 3334)	Novel Protein sim. GBank gj5689535[bj]BAA83051.1] - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein [for Arf]	transport	264259, 29331822, 29331828, 264905, 264908, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264766, 264688, 21906765, 21906767, 21906769, 265020, 265021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gj2076894[gb]AAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE- bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264889, 33657109, 35696423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gj3875371[emb]CAA85414.1] - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit: cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33109954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gj462451[sp]P34244[KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906768, 21906769, 264691, 264555, 264556, 22279000, 264566
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gj1814270 (U74586) - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	264906, 264909, 264632, 18108381

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gj 2076894 gb AAB53983.1 - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33857023, 264692, 264693, 33557109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gj 5262467 emb CAB45693.1 - (AL080062) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 264906, 52644045, 60433356, 87168559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gj 3128366 (AF010496) - 50S ribosomal protein I9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gj 4164065 gb AAD05327 - (AF111091) latrophilin 3 splice variant bbaa [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gj 3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	8686829 (3355, 3356)			UNCLASSIFIED	29331824, 264102
1679	91214106 (3357, 3358)	Novel Protein sim. GBank gj 550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gj 2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gj 5689537 dbj BAA83052.1 - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gil5031717ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264692, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gil1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424179, 52646842, 22278984, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gil2244707 dbj BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264567
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gil4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gil4240193 dbj BAA74875.1 - (AB020559) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gil3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264369, 21906766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gil2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gil121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_006225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	mapolymerase	35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29146499, 264905, 264908, 52644045, 264511, 265008, 265007, 265009, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 264692, 264693, 18108370, 18108374, 263978, 35696423, 35695855, 264558, 18108381, 18108385, 87168518, 264482, 264486 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21906766, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21906769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002 35696286, 264635
1699	87424793 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir IS41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED nucl_recpt	29331824, 52644045, 265008, 265009, 263969, 263971
1700	87859161 (3399, 3400)				
1701	86570488 (3401, 3402)				
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi 3877439 emb CAA96652 - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	264092, 264110, 263977 22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263978, 35695855, 264555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1704	86622978 (3407, 3408)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264369
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264807, 265010, 264687, 264768, 264892, 264693, 264636, 264566
1706	87790967 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21908768, 21906769, 265022, 264691, 264558, 22279000

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gij4321664[gb AAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108398, 22278997, 264259, 29147620, 29331826, 29146498, 284905, 284906, 285008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35696423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gij5174591[ref NP_005947.1 pMTHF - 5,10-methyltetrahydrofolate dehydrogenase, 5,10-methyltetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265018, 18108351, 264448, 21906765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	284556
1711	81013729 (3421, 3422)	Novel Protein sim. GBank gij5031735[ref NP_005760.1 pHEC- - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gij5454168[ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 284683, 264686, 264689, 265020, 33657023, 263967, 33657109, 263974, 35696423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gij160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278995, 284508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21906765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gij5689537[dbj BAA83052.1 - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264807, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264584
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gij4589468[dbj BAA76761.1 - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 284600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749 - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264688, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14999 Y076 HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 2279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 56182181, 66714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182323, 264559, 264564, 264486, 56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	22278994, 22278999, 29331822, 265006, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1 - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5689375 dbj BAA82968.1 - (AB030644) tudor repeat associator with PCTAIRE 2 [(Rattus norvegicus)]	Contains protein domain (PF00567) - Tudor domain	kinase	

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi 4426962 gb AAD20633 - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33658970, 33657349, 29146499, 264508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432229, 264582, 60433358, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264567, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi 2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi 3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264568
1726	85754255 (3451, 3452)			UNCLASSIFIED	29146498, 264683, 264689
1727	85286362 (3453, 3454)	Novel Protein sim. GBank gi 4689348 gb AAD27861.1 AF13256 - (AF132562) BcDNA LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21908768

1728	95349515 (3455, 3456)	Novel Protein sim. GBank gij4406549[gb AAD20027] - (AF131738) Unknown [Homo sapiens]		UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56954075, 35696286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)			UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266068 (3461, 3462)	Novel Protein sim. GBank gij631600[pr]S47094 - hypothetical protein - rabbit		UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gij4240231[dbj BAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]		struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PID).	- synthase	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264636, 264556
1734	87795261 (3467, 3468)				264693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gil4836807[gb]AAD30566.1[AF146793] PF127 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 284689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gil4885647[ref]NP_005472.1[pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gil2143607[pir][S68695 - BIK protein - rat	Contains protein domain (PF00168) - C2 domain	kinase	29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gil222594.1[emb]CAA69714] - (Y08460) Mdes protein [Mus musculus]		UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gil4809[emb]CAA44309] - (X62452) YCR601 [Saccharomyces cerevisiae]		traffic	264604, 21906764, 18108364, 264629, 35695855, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gil4883898[gb]AAD31695.1[AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gil4505193[ref]NP_003667.1[pMLD] - membrane fatty acid (lipid) desaturase		UNCLASSIFIED	264906, 264910, 264758, 265011, 264631, 264638, 264566
1743	85966475 (3485, 3486)				265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gil728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII		UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)			UNCLASSIFIED	264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gil731756[sp]P38873[YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK11 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gil1658503 (U75467) - Alu [Drosophila melanogaster]	transcript factor		52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3485, 3498)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00694) - DnaJ central domain (4 repeats)	- eph	264489, 56182375, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811578, 264635, 264555, 264556, 264557, 264559
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AAD45948.1 AF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	264106
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi 4996894 gb AAC28444.2 - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			33657402, 264288, 52644150, 263974, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 dbj BAA24184 - (AB010054) outer arm dynein light chain 2 [Anthracidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase associated	265010, 264369
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3915482 sp P74346 YG29_SYNY3 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylation synthase	deaminase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acytransferase	phosphatase	56994075, 22278996, 264908, 60170831, 284682, 264784, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39981 YEHA_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION		transport	264488, 35696286, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 284604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567 264686
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	92962614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33856970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CAB46856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_bind	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3516)	Novel Protein sim. GBank gjl3881040[emb]CAA16403] - (AL021497) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265008, 265007, 265009, 264591, 33657402, 33109954, 87169474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52844332, 22278002, 264563
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gjl5262748[emb]CAB45688.1] - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432048, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432228, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gjl127749[sp]P10569[MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gjl3169158 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gjl4809026[gb]AAD30062.1] - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gjl1360669[pir]CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 80432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gjl486806[pir]IS35503 - finger protein neuralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21908766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	85081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	52645156, 87168559, 60170615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755988 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1 - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]			UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)				UNCLASSIFIED	29331824, 29331825, 264591, 56182323 264563
1769	87388988 (3537, 3538)				UNCLASSIFIED	264488, 264768, 264769, 56182575, 55811957, 264690, 264891, 35696052, 264905, 264509, 264806, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264768
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin		complement	
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914191 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain		transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHHC zinc finger domain			22278998, 29331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495699 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	85359330 (3549, 3550)	Novel Protein sim. GBank gij1459189 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35686052, 29331830, 66712502, 264826, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	84133756 (3551, 3552)	Novel Protein sim. GBank gij4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gij3219939 sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1		nucd_recpt	56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	84851624 (3555, 3556)	Novel Protein sim. GBank gij3875648 emb CAA91454.1 - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	84133758 (3557, 3558)	Novel Protein sim. GBank gij4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264766
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gij729225 sp P41237 CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264563
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gij2257543 dbj BAA21436 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	85197093 (3567, 3568)	Novel Protein sim. GBank gi 1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 56712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264369, 264766, 264687, 264768, 264688, 21906768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264565, 264566, 264486
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi 4589552[dbj BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21906767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1786	85296485 (3571, 3572)	Novel Protein sim. GBank gi 117788[sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)	UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 3877175[emb CAA90338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264808, 264595, 264764, 264766, 264692, 60431528, 264628, 264636, 264564, 264566
1788	91228779 (3575, 3576)		UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gi 2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264638
1790	82489734 (3579, 3580)			35696052, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1781	95187258 (3581, 3582)	Novel Protein sim. GBank gi 2114321 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264884, 264567, 18108354, 18108391, 264685, 264766
1782	87782690 (3583, 3584)	Novel Protein sim. GBank gi 4337106 gb AAD18082 - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33657402, 87188559, 264368, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1783	95337877 (3585, 3586)	Novel Protein sim. GBank gi 5579331 gb AAD45504.1 AF14573 - (AF145732) endoplasmic reticulum alpha-mannosidase 1 [Homo sapiens]	Contains protein domain (PF01532) - ATPase associated Glycosyl hydrolase family 47	ATPase associated	65274572, 22278995, 22278996, 22278997, 22278999, 264093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52844150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1784	87759806 (3587, 3588)	Novel Protein sim. GBank gi 4914604 emb CAB43677.1 - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snoRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264783, 264448, 264683, 264369, 21908765, 21908766, 21906767, 21906769, 29148784, 35695917, 60170615, 33657023, 264629, 18108374, 18108378, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264564
1785	79747856 (3589, 3590)			UNCLASSIFIED	264632, 264635, 264638, 264595, 264596, 264907, 264566, 264909
1786	86598486 (3591, 3592)	Novel Protein sim. GBank gi 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	264488, 264907, 264909, 264594, 264595, 264766, 264687, 21906765, 21906767, 264628, 264630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gi 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21908754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gi 2832906 dbj BAA24608.1 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21908754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906768, 21906767, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gi 5689541 dbj BAA83054.1 - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21908769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	264691, 264556, 264566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21906769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264596, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gi 3879914 emb CAA98538.1 - (Z74043) predicted using GeneFinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gi 5453644 ref NP_008461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52844229, 35696423, 264636, 60432113
1808	94133762 (3611, 3612)	Novel Protein sim. GBank gi 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35696423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gi 4884079 emb CAB43235.1 - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696286, 66714117, 35696052, 66712502, 284592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gi 1916027 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264558, 264557, 264558
1810	88096316 (3619, 3620)	Novel Protein sim. GBank gi 1352944 sp P47179 YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35696052, 264905, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gi 2134984 pir J37275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - kinase Ank repeat		264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 284483
1812	79245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21906769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 66714117, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906766, 21906768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264559, 22279000, 22279002, 264566
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264092, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		struct	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176623 sp P41846 YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi 3766377 emb CAA21429 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52844150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 3879121 emb CAA94370 - (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcript factor	35696286, 60433356, 264758, 264369, 264686, 21906769, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264567

1820	87769455 (3639, 3640)				284905, 264907, 264594
1821	80431510 (3641, 3642)				264907, 264768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1 - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35696052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264596, 265017, 265019, 18108351, 264763, 264683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 264693, 35696423, 264634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284907, 264908, 264909, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264566
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gi 3036803 emb CAA18493 - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi 4680685 gb AAD27732.1 AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase_associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35696052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644298, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170615, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gll4503571[ref]NP_001419.1pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52646842, 56182575, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265008, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433358, 60433438, 264758, 33109954, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264688, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263872, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35696423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265018, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gll1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8.....			264602

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gil5174413[ref]NP_006026.1 pCDC4 - CDC42-binding protein Kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein Kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 264509, 264908, 264907, 66712502, 264908, 52644045, 264909, 264512, 265008, 264591, 264593, 60433356, 21906754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264768, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27486264, 33657349, 65274791, 264634, 264635, 264558, 264557, 264558, 264559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)				264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21906768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gil4759288[ref]NP_004268.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gil3334400[sp]Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gil1362599[pir]A56154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gil2117310[emb]CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gil127560[sp]P23249 MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gil4572464[gb]AAD23834.1 AF12365 - (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	9092645 (3683, 3684)	Novel Protein sim. GBank gi 1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108384, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 284691, 60432229, 60432049, 264258, 264629, 33657023, 264486, 264909, 264567, 264595, 264766
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi 1175494 sp Q09819 YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21906765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi 3881080 emb CAA21739 - (AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gi 5059323 gb AAD38967.1 AF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi 5701854 emb CAB52191.1 - (AJ245417) G5b protein [Homo sapiens]		Im7	29331825, 29331826, 29331827, 265017, 264683, 264288, 264766, 264768, 21906767, 21906768, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi 4503665 ref NP_001989.1 pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi 4589582 dbj BAA76813.1 - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi 220637 dbj BAA01477 - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35696052, 264910, 60433438, 264688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gij5174629[refNP_006090.1]pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22278002, 264563
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gijB54065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645128, 29331827, 33656970, 33657349, 35695763, 264508, 264906, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264834, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gij2072964 (U93569) - putative p150 [Homo sapiens]		nuclease	264592
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gij4539520[emb]CAB39994.1] - (AL035424) dA22D12.1 (novel protein similar to Drosophila Keich (Ring Canal protein, KEL) and a heterogenous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Keich motif	- nucl_recpt	18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gij3954978[emb]CAA06945] - (AJ006278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gij4322670[gb]AAD16120] - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase_associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	264757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			22278996, 29331824, 265007, 33109954, 265019, 264369, 21906768, 29148784, 27486261, 52644332, 22278002
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi 4009522 (AF099731) - connexin 31.1 [Homo sapiens]			265019
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir J184505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 264259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 264686, 264691, 264893, 27486264, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 264259, 87168474, 264369, 21906768, 264558, 264583
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CAA09299 - (AJ010642) Dof protein [Drosophila melanogaster]		UNCLASSIFIED	264601, 264766, 29148627, 29148629, 264692, 264629, 264835
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 4322263 gb AAD15985 - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278999, 264259, 264907, 265018, 18108370, 264634, 264635, 264555, 264556, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2495727 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278999, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265019, 264760, 264448, 264768, 29148627, 29148629, 265020, 265022, 18108385, 60432113
1866	87268816 (3731, 3732)	Novel Protein sim. GBank gi 5262617 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21906769, 29148629, 35696286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 264555, 264691, 264259, 264556, 264692, 264557, 33657023, 60433356, 29331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	264094

1868	87357459 (3735, 3736)	Novel Protein sim. GBank gi 3881525 emb CAA93884 - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 27486264, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264568, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gi 4826772 ref NP_004961.1 p GFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leuchne Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 284883, 264768, 264769, 35695855, 284634, 284558, 264639, 18108385, 264583, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gi 1869859 emb CAB06722 - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424259, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108388, 35695763, 35696423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264583, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264567, 264766
1875	87330515 (3749, 3750)	Novel Protein sim. GBank gi 4589520 db BAA76782.1 - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi 263810 bbs 122920 - collagen alpha chain [Riftia pachypila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi 3983356 gb AAC83924.1 - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gi 4510345 gb AAD21434.1 - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35696286, 56994075, 264259, 29331822, 29331824, 29331825, 35698052, 29331826, 29146498, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264369, 264288, 264766, 264687, 264768, 264769, 21806768, 35695917, 265021, 60170615, 33657023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264564, 264566, 264488, 264567, 264905, 264907, 264908, 265007, 264565, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gi 1550785 emb CAA69283 - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gi 93144 pir B40505 - hypothetical protein - suld herpesvirus 1 (strain Indiana-Funkhuser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gi 2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21806766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	hameobox	264908, 264910, 87168559, 21906766, 264638

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gil4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181586, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811386, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264882, 264763, 264883, 264764, 264288, 264369, 264768, 264686, 264768, 264769, 29148784, 35695917, 264690, 264891, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gil2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gil2854158 gb AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gil5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gil3318931 emb CAB10841 - (Z98046) dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gil1083308 pir A56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21906768, 21906769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gil4240195 dbj BAA74876.1 - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)				UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gi 5689535 dbj BAA83051.1 - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct		22278995, 264508, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin		264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 265008, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264766, 264687, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)					264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264638, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gi 5262574 emb CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat			56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 56182323, 56526486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED		264907, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!		cadherin		264259
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase		22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gi 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein		264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3789, 3800)	Novel Protein sim. GBank gi 4102861 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED		264683

1901	95196847 (3801, 3802)	Novel Protein sim. GBank gij585959[sp]P38378[S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52648842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432048, 264259, 29331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264908, 264907, 29331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21908754, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264886, 52644229, 21908765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 263987, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35698423, 35695855, 60431850, 264638, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264584
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gij4426613[gb]AAD20451] - (AF098798) SLM-1 [Mus musculus]		dna_ma_bind	264107, 263976
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21906754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911[sp]P47147[YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264908, 264907, 264908, 265007, 264910, 264688, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264585
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714[dbj]BAA25521] - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35698423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1906	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21908754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906768, 21906768, 265020, 265022, 264690, 52844150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264805, 264906, 264907, 264908, 66712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264686, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 28148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264568, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264768, 264768, 264687, 264769, 35695917, 265021, 52844150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC00653 - (AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264906, 264907, 264908, 52644045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264566
1913	95305546 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3828, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1 - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gij5689391[dbj BAA82979.1] - (AB028950) KIAA1027 protein [Homo sapiens]		struct	264769, 264689, 21906765, 21908768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264905, 264906, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264638, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264568, 264764, 264766
1918	85302795 (3835, 3836)	Novel Protein sim. GBank gij5281517[gb AAD41524.1 AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21908769, 22278994, 35696288, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657108, 29331826, 52845129, 35696052, 29331828, 27486282, 27488264, 35695763, 264508, 264905, 264509, 264906, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264834, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264598, 83373044, 264758, 52646317, 18108385, 52644296, 56526486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264805, 264760, 264761, 264482, 264564, 18108351, 264762, 264682, 264565, 264448, 264784, 264566, 264486, 264567, 264369, 264288, 264766, 264487, 264585
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gij3878584[emb CAB01237] - (Z77667) cDNA EST EMBL:C08125 comes from this gene; cDNA EST EMBL:C09753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gij1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264566
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gij4580997[gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 MT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	84323589 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35696052, 264509, 264905, 264908, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 5581150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35696423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264585, 264566, 264567 29331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA86657 - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		snuct	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264892, 264693, 263978, 264631, 264634, 264637, 264583
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi 3043632 dbj BAA25480 - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87799054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 dbj BAA13377 - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf Extracellular link domain	Inf	264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gil1709230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35695286, 29331828, 264905, 264907, 264808, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264805, 264760, 264764, 264766, 264686, 264769, 265022, 35695423, 264638, 60432113
1931	87797279 (3861, 3862)	Novel Protein sim. GBank gil404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00068) - Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264634, 264637, 264684, 264691, 264635
1932	15030972 (3863, 3864)			UNCLASSIFIED	264595
1933	11613668 (3865, 3866)	Novel Protein sim. GBank gil4115748 dbj BAA36494] - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 264510, 264757, 264758, 55812038, 55811386, 265018, 55811150, 21906765, 264691, 264631, 264635, 264637
1935	87752511 (3869, 3870)			UNCLASSIFIED	264686, 265011, 264511, 264905, 18108351, 264564, 264681, 264259, 18108370, 264566, 264764, 264369, 264595
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gil4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			60432289, 265007, 265010, 265011, 265019, 33657109, 18108374
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gil543187 pir S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35695917, 60170615, 264693, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gil4544431 gb AAD22340.1 AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 28146498, 264905, 264559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gil500858 dbj BAA03210] - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906766, 21906768, 55811957, 27486264, 35696423, 60432113, 264564
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gil1946300 emb CAA73132] - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1941	94147177 (3881, 3882)	Novel Protein sim. GBank gil4206386 (AF060570) - fig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21906765, 21906766, 21906767, 265020, 52644150, 27486264, 83373044, 18108387, 60432113, 22279002, 264565
1942	87641870 (3883, 3884)	Novel Protein sim. GBank gil4927204 gb AAD33049.1 AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
1943	94325298 (3885, 3886)	Novel Protein sim. GBank gil3122952 sp O15736 TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 264511, 265009, 264592, 60432229, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264636

1944	84232958 (3887, 3888)	Novel Protein sim. GBank gij1799570[dbj BAA13432] - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432228, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906768, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563, 264488, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1945	87641872 (3889, 3890)	Novel Protein sim. GBank gij4927204[gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	
1946	87443980 (3891, 3892)	Novel Protein sim. GBank gij2498104[sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52844150, 264693, 27486264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gij3914801[sp O54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		mapolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gij5420387[emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		struc	264909, 60170831, 264591, 264594, 265010, 265011, 264764, 264369, 264689, 264631, 264638
1949	7640129 (3897, 3898)				264369
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gij3876766[emb CAA93466.1 - (Z69637) predicted using Genefinder, Similarity to E. coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gij2626753[dbj BAA23424 - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gij4929633[gb AAD34077.1 AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264585

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gij1168715 sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558
1954	9126025 (3907, 3908)	Novel Protein sim. GBank gij4240271 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35696286, 22278998, 29331822, 66714117, 29331826, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 265007, 265008, 264910, 265008, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264768, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 284508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21908765, 21908768, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27488284, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 284635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gij1665821 dbj BAA134071 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1857	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA76856.1 - (AB023229) KIAA 1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278987, 22278998, 22278999, 29331824, 68714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33657349, 27486265, 35895855, 22279002, 264482
1858	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020878) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264092, 264094, 264259, 60432049, 29331824, 56182181, 68714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 265010, 21906769, 35895917, 265022, 65274620, 263967, 263976, 35696423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002
1859	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860 - (Z98056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	264593, 265019
1860	80308608 (3919, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515 - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264806, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21906765, 18108368, 264629, 18108379, 264635, 264636, 264637, 264638, 264486
1861	16292607 (3921, 3922)				264635
1862	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1863	90936017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581 - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432289, 29331827, 264828, 265008, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486265, 35695855, 264555
1864	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1 - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264584, 264565, 264566, 264486, 264567
1865	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294 - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	94192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - glycoprotein Uncharacterized protein family	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264488, 264567
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - esterase Phosphatidylinositol-specific phospholipase C, X domain	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain	35685286, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264882, 264764, 264885, 264768, 264767, 264889, 264691, 264693, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]	UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]	UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134208 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR	collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264807, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21906765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264585, 264586, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 dbj BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain	22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644296, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)		UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MILL [Fugu rubripes]	UNCLASSIFIED	264682, 264764, 264563

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265008, 284757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 35895855, 58182323, 60432113, 264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1976	95358914 (3951, 3952)			UNCLASSIFIED	264908, 264596, 265021, 264566
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gi 2499528 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 103421 pir J A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcriptfactor	60170831, 264568
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1 - (Z97336) hypothetical protein (Arabidopsis thaliana)		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759280 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406693 gb AAD20060 - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264908, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	80995367 (3963, 3964)	Novel Protein sim. GBank gi 5689523 dbj BAA83045.1 - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811388, 264760, 264686, 264691, 27486264
1983	95098688 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1984	85760989 (3967, 3968)	Novel Protein sim. GBank gjl2896695[embjCAA17174.1]- (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21908766, 55811957, 56994075, 265020, 265021, 22278999, 265022, 284259, 29331822, 33657182, 29146499, 264628, 18108370, 264908, 264629, 55811576, 35695855, 265008, 265007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gjl5712131[gbjAAD47379.1]AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264564
1986	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gjl4868443[gbjAAD31319.1]AF14457 - (AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21908768, 33657023, 264692, 264693, 18108377, 264635, 60170394, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gjl2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85699888 (3979, 3980)	Novel Protein sim. GBank gjl5701727[dbjBAA83074.1]- (AB024729) alpha-1,3-D-mannoside beta-1,4-N- acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gjl4240287[dbjBAA74922.1]- (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35696286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264486
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gjl2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	29331827, 264906, 264807, 264909, 265007, 264603, 264766, 264686, 264768, 21906768, 264628, 264635, 264636, 18108385, 56526486, 264566, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gjl2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264564 264488, 18108396, 22278994, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 284764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148527, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811578, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87168518, 264404, 60432113, 264567 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit	UNCLASSIFIED		
1996	80254185 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020 - (X86028) extensin-like protein [Vigna unguiculata]	UNCLASSIFIED		
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 dbj BAA76839.1 - (AB023212) KIAA0995 protein [Homo sapiens]	UNCLASSIFIED		264113, 264685, 264555, 264567

1999	94324903 (3997, 3998)	Novel Protein sim. GBank gi 5225312 gb AAD40846.1 AF07244 - (AF072441) calchneurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486284, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gi 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27486261, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi 107560 pir JB38637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi 729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gi 86388 pir JA27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1 - (AL049996) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645158, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483, 264488, 264906
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613 - (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 66714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482, 264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264539, 264566
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gi 3882305 dbj BAA34512.1 - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264681, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gi 5262629 emb CAB45753.1 - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	eph	52844507, 52845158, 52846365, 52846842, 18108397, 65274572, 22278994, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52646317, 33109954, 52844296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263987, 52845129, 35695763, 18108376, 35696423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264564, 264565, 264566, 264567, 56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gi 3347953 AF076183 - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gi 1086678 U41020 - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin tight chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi 4507885 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pIZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gi 127720 sp P20938 MYP0_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	264488, 29331826, 264907, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gij181286 pir S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264628, 35698423, 35695855, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij265046 pir S26413 - t-complex protein Tcp-10 - mouse		struct	264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33657109, 27488282, 263972, 18108374, 263976, 264555, 264564 264685, 264636
2017	79464293 (4033, 4034)			UNCLASSIFIED	264693
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gij124735 sp P18175 INVO_PIG - INVOLUCRIN			
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gij2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gij585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21908768, 33657023, 33657109, 27486261, 87168518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gij5410230 gb AAD42992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264782, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2024	87896443 (4047, 4048)				60433438, 265017, 264686, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gij4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170615, 264556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gij1655699 emb CAA69032 - (Y07752) pterophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gjl1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 284757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 56526486, 22279000, 22279002, 264563
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gjl3599940 (AF017368) - (faciogenital dysplasia protein 2 [Mus musculus])	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	285009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gjl5630080 [gb AAD45825.1 AC00489 - (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)				264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gjl5689491 [dbj BAA83029.1 - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906766, 21906767, 29148627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gjl2484828 [sp Q64686 CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		synthase	56181562, 264628, 264632, 264555, 264556
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gjl4826984 [ref NP_005147.1 pR0D1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 284907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 284632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi 3880625 emb CAB07858 - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 284692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	85514626 (4077, 4078)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 284634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi 2500625 sp P70700 P70700_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 406590 gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264258, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 284595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21906765, 35895917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35696423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264583, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF14563 - (AF145632) [BcDNA.GH06032 [Drosophila melanogaster]]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		strut	264093, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21906769, 265020, 264692, 264482, 264566
2045	79635532 (4089, 4090)				264682
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 406698 gb AAD20062 - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22279002
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gi 4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gi 4589656 dbj BAA76850.1 - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264564, 264565, 264566, 264567

2050	79633835 (4099, 4100)				264693	264488, 264259, 264509, 264906, 264907, 264769, 18108374, 35696423, 264563, 264566, 264486
2051	87780168 (4101, 4102)				UNCLASSIFIED UNCLASSIFIED	
2052	88086393 (4103, 4104)	Novel Protein sim. GBank gi 4529889 gb AAD21812.1 - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain		UNCLASSIFIED	264488, 263994, 35696052, 284508, 264905, 284509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 284592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 284630, 284631, 264632, 264634, 284635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567, 264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 284910, 60170831, 284592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264768, 284688, 284768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 284630, 264631, 264632, 264634, 264635, 264636, 264566, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi 2995449 emb CAA75113 - (Y14848) midline 1 protein [Mus musculus]			UNCLASSIFIED	22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482, 60424179, 264094, 264259, 29331825, 60424269, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi 3876326 emb CAB02090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			264488, 29331825, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi 5353746 gb AAD42226.1 AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]			UNCLASSIFIED	

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gi 4826980 ref NP_005042.1 pQARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - synthase tRNA synthetases class I (E and Q)	264488, 52645156, 56182575, 22278994, 35698286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264908, 264908, 265006, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21906754, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264369, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486261, 27486264, 27486265, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264568, 264567, 52646842, 52646365, 56182575, 35698286, 22278996, 22278997, 22278998, 264093, 52645080, 35698052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	UNCLASSIFIED	265007, 265008, 264591 29331825, 264682, 264686, 264691, 264693, 22279002
2058	86276896 (4115, 4116)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576
2059	79866684 (4117, 4118)	Novel Protein sim. GBank gi 2811122 (U87318) - NaDC-2 [Xenopus laevis]	UNCLASSIFIED	
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gi 2811122 (U87318) - NaDC-2 [Xenopus laevis]	UNCLASSIFIED	

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56528486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	strucl	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 26487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 dbj BAA76803.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 dbj BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264881, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264764, 264288, 56182323, 264567
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	

2067	95303892 (4133, 4134)				35686286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264563, 264486
2068	84344754 (4135, 4136)			UNCLASSIFIED	264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656970, 264509, 264905, 58182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gij5712131[gb]AAD47379.1[AF12049 - (AF120499)] DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264905, 284628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gij3551531[dbj]BAA33016[- (AB017437)] avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 284634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophysial hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gij1504026[dbj]BAA13212[- (D86976)] similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gij4240317[dbj]BAA74937.1[- (AB020721)] KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264557

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gi 5138930 gb AAD40382.1 - (AF093880) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33857084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)		UNCLASSIFIED		264592
2078	87539364 (4155, 4156)	Novel Protein sim. GBank gi 4220590 db BAA74579 - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger		29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gi 4240255 db BAA74906.1 - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264906, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gi 2408021 emb CAB16219.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gi 5524734 gb AAD44360.1 AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gi 3880558 emb CAA94234 - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21908754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - III! ALU SUBFAMILY SP WARNING ENTRY III!		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) perophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264688, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936 - (Z49125) similarity to Trichostromytilus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35696423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880930 emb CAA16334.1 - (AL021481) similar to Phosphoglucosyltransferase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36166 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...			264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35696423, 35695855, 83373044, 87168518, 22279000, 264567, 18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33659970, 29146498, 29146499, 284102, 284106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 284828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21906754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 284761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264688, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148629, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690,
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin		

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 284910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000, 263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811388, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gi 4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi 1363238 pir A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94118760 (4191, 4192)	Novel Protein sim. GBank gi 3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278996, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52844150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gil5174501ref[NP_006051.1]pLYF1 - zinc finger protein. subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264692, 33657109, 18108370, 264636, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gil4758208ref[NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gil2695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gil3881189[emb]CAB16514] - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc_recpt	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21906754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gil4589468[dbj]BAA76761.1] - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gil3874149[emb]CAA97423.1] - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21906769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gil4240159[dbj]BAA74858.1] - (AB020642) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21906765, 21906768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264584
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gij1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56984075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33857084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264584, 264566, 264567
2106	83365475 (4211, 4212)				265006, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gij3881524[emb]CAA93883] - (Z70038) ZK1067.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gij3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264835, 264638, 264639, 83373044, 264486
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gij481043[pri]S37671 - bat2 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)			UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gij2143639[pri]I56542 - calmodulin-binding protein - rat	Contains protein domain (PF00069) - struct		264508, 264906, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gij426629[gb]AAD20459] - (AF100960) protocadherin [Rattus norvegicus]	Eukaryotic protein kinase domain Contains protein domain (PF00028) - cadherin Cadherin domain		265006
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gij3327184[dbj]BAA31660] - (AB014585) KIAA0685 protein [Homo sapiens]			66714117, 29331826, 28331827, 60433438, 55812038, 265017, 265019, 264689, 21906769, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gij4757890[ref]NP_004328.1pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264688, 264691, 264692, 60432113

2116	88259387 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35696286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 264907, 56182435, 265008, 264591, 55812038, 55811386, 87168559, 264288, 264369, 21906769, 29148629, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP, Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1078307 [pir][B56573 - nuclear pore complex glycoprotein p62 - African clawed frog]		glycoprotein	264259, 264805, 264807, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264768, 264893, 263967, 263972, 264638, 264559
2119	86989317 (4237, 4238)	Novel Protein sim. GBank gij4321407 [gb][AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gij4885527 [ref][NP_005480.1] pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij475728 [ref][NP_004886.1] pAGTA - angiotensin/vasopressin receptor All/AVP-like		UNCLASSIFIED	264601, 264766, 263978
2122	91230931 (4243, 4244)	Novel Protein sim. GBank gij4929551 [gb][AAD34036.1] pAF15179 - (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 264565, 264567
2123	86787898 (4245, 4246)	Novel Protein sim. GBank gij2224551 [dbj][BAA20764] - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108396, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5689455 [dbj][BAA83011.1] - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264906, 264907, 264591, 264639, 264563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gij728831 [sp][P39188] ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY !!!		UNCLASSIFIED	264259, 264509, 264907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539264 [emb][CAB39853.1] - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264601, 264603, 265018, 264804, 264605, 264760, 264681, 264762, 264883, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gi 4868435 gb AAD31315.1 AF14323 - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35696286, 29331826, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 284635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 55182575, 35696286, 56182181, 29331824, 60432289, 35698052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 284288, 264369, 264687, 264788, 55811957, 284692, 18108388, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000
2129	95102089 (4257, 4258)			UNCLASSIFIED	263981
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gi 2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gi 1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	potassium_channel	35696052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gi 5689373 dbj BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 284288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21906769, 284690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gi 4220489 (AC060609) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 35696286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812036, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 58181562, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gi 3875351 emb CAB09415 (Z96047) DY3.6 [Caenorhabditis elegans]			56181688, 35696286, 21906754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21906768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gi 5689559 dbj BAA83063.1 (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22279999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87188559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gi 4884110 emb CAB43262.1 (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264763, 21906768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gi 5174779 gb AAD40696.1 (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase-associated	264259, 29331828, 35696052, 264909, 265008, 265017, 265018, 18108351, 264288, 21906768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gi 3850821 emb CAA77135 (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]			264905, 264910, 264591, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108384, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gi 4417293 gb AAD20418 - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264759, 265018, 264448, 264288, 21906768, 55811957, 265021, 33657023, 27486265, 35696423, 264636, 264556, 264557, 264559, 264566
2141	78623986 (4281, 4282)			UNCLASSIFIED	265020, 284893
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi 2135766 pir S53362 - mucin SAC (clone JER47) - human (fragment)		UNCLASSIFIED	22278997, 29331827, 284907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 65274791, 22279002
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi 1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264909, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gi 3080398 emb CAA18718.1 - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gi 119863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - glycoprotein Lectin C-type domain		29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]			22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906766, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase		18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gil4758704[refNP_004216.1]pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264780, 264288, 264369, 264766, 264687, 264769, 52644229, 21906768, 21906768, 35695917, 33857023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gil225150[prfj1209265U - chorlon protein B11 [Bombyx mori]]		UNCLASSIFIED	56994075, 264084, 265009, 265019, 264288, 21906767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gil3970966 (AC004974) - spa-1- like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)				264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gil1076211[prfjS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gil4650844[dbjBAA77027.1] - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gil2879825[dbjBAA24826] - (AB007897) KIAA0437 [Homo sapiens]			264634
2161	87739131 (4321, 4322)			UNCLASSIFIED	265008
2162	94319526 (4323, 4324)	Novel Protein sim. GBank gil1504006[dbjBAA13202] - (D86966) simlarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gil3876537[embjCAA98270] - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gi 1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 29331828, 264906, 29331830, 58182435, 265009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22278998, 66714117, 52645158, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526486, 87168518, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gi 2706522[embjCAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]		ubiquitin	56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35698423, 18108381, 18108384, 18108385, 60432113, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gi 2224713[dbjBAA20840] - (AB002384) KIAA0386 [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35698423, 18108381, 18108384, 18108385, 60432113, 264567
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gi 4321407[gbjAAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264568
2169	87886937 (4337, 4338)				264629, 264555, 264559
2170	94141033 (4339, 4340)	Novel Protein sim. GBank gi 5106521[gbjAAD39741.1]AF10536 - (AF105365) K-Ci catransporter KCC4 [Homo sapiens]		UNCLASSIFIED	55274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	67036740 (4345, 4346)	Novel Protein sim. GBank gi 4309681[gbjAAD15478] - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gi 2493778[sp Q09456]YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5			264906, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi 1263287 (U47855) - fibroin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21906788, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!! ALU SUBFAMILY SQ WARNING ENTRY !!!	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52844296, 87168559, 265018, 264689, 21908785, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52845129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gi 5454072 ref NP_006416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi 473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424269, 264760, 264628, 264632

2180	95351397 (4359, 4360)	Novel Protein sim. GBank gil3122317 sp P90648 KMH8_DICD1 - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52844150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22278000, 264482, 264568, 264567, 264486 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gil3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gil5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22278000, 22279002 264760
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gil3873406 gb AAC77482.1 - (U17129) unknown [Rhodococcus erythropolis]			
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gil3114713 (AF061346) - Edp1 protein [Mus musculus]		tnf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557 29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gil5106956 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gil2864625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]		ATPase_associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 284766, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264568, 264486 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gil5107816 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850. Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gil3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263967

2190	87639197 (4378, 4380)	Novel Protein sim. GBank gj 132575 sp P29315 RNI_RAT - RIBONUCLEASE INHIBITOR			nucleaseinhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644298, 265010, 265018, 264685, 264688, 56181562, 21908769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gj 5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]				29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gj 462600 sp P34400 MI10_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain			264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gj 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810784, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gj 2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]				264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gj 2832763 emb CAA15685.1 - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /motif=(desc: [Drosophila melanogaster]			UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gj 5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]			collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21908766, 21908767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264638, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gj 4929567 gb AAD34044.1 AF15180 - (AF151807) CGI-49 protein [Homo sapiens]				264768, 264769, 21906765, 21906766, 21906767, 29148627, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21908754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88060914 (4395, 4396)	Novel Protein sim. GBank gj 3548787 (AC005622) - R30953.1 [Homo sapiens]			UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gi 2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4389, 4400)	Novel Protein sim. GBank gi 3043634[db][BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct		29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gi 3913470[sp]O57314[DHXB_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2]	dehydrogenase	Contains protein domain (PF00106) - short chain dehydrogenase	29331824, 35696052, 264905, 264907, 33857402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gi 5262665[emb][CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 284448, 264369, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gi 172845[sp]P46629[R825_RABIT - RAS-RELATED PROTEIN RAB-25]	glycoprotein	Contains protein domain (PF00071) - Ras family	52646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168558, 265018, 265019, 264605, 284288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88086671 (4407, 4408)	Novel Protein sim. GBank gi 121036[sp]P29348[GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT, (GUSTDUCIN ALPHA-3 CHAIN)]	UNCLASSIFIED	Contains protein domain (PF00503) - G-protein alpha subunit	
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gi 4589480[db][BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	dna_rna_bind	Contains protein domain (PF00096) - Zinc finger, C2H2 type	18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 80432228, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108368, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566, 264591
2206	20620008 (4411, 4412)		UNCLASSIFIED		264591
2207	87787970 (4413, 4414)	Novel Protein sim. GBank gi 4557753[ref]NP_000372.1[pmid]1 - midline 1 protein		Contains protein domain (PF00622) - SPRY domain	29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264568, 264906, 265019, 18108351, 21906769, 264112, 265009, 264691, 18108365, 18108374, 264634, 20281166
2208	86100830 (4415, 4416)				
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gi 3986746 (AF105228) - tuftelin [Bos taurus]	struct		

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 264082, 264094, 29331822, 66714117, 29331826, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644229, 21906765, 21906768, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264558, 264637, 264558, 83373044, 22278002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gi 4504325 ref NP_000173.1 pHADH - hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433358, 60433438, 33109954, 33657084, 52644298, 87188474, 265010, 265011, 87188559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 284288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108384, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526488, 87188518, 60432113, 22279002, 264482, 264564, 264565, 264566, 264909, 265006, 264555, 264558, 87188518
2215	95419206 (4429, 4430)	Novel Protein sim. GBank gi 1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]			
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		UNCLASSIFIED	264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gi 5031707 ref NP_005503.1 pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gi 3878636 emb CAA88953 - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		35696423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family		264682, 264683, 264688, 264689, 264693, 18108370, 18108378

2220	85354165 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - statherin			264488, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 85658542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264764, 264369, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84789 - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265006, 265008, 265009, 264757, 21906754, 18108351, 264693, 18108374, 18108385
2225	85748484 (4448, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52644045, 264600, 265019, 21906765, 21906769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CAB42852.1 - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 284486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148629, 29148784, 27486261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264091, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gij226154[prf]1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278998, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328.1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316[gblAAD41476.1]AF13312 - (AF133124) transcription factor IIC63 [Homo sapiens]		transcriptfactor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264690, 52844150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4249733[gblAAD13780] - (AF109377) IdIBp [Mus musculus]			
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559[sp]P54352[EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)]		kinase	56182435, 264369, 264688, 21906765, 265020, 264693, 264556, 56526486
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gij4972734[gblAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675[pir]B53814 - p20 protein - human	Contains protein domain (PF00011) - eph Hsp20/alpha crystallin family		264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 284906, 284907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734[gblAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	84998857 (4475, 4476)			Contains protein domain (PF00286) - Viral coat protein		264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)					29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gij2882311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]		Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 65274572, 56182575, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21906765, 21908768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)				UNCLASSIFIED	254693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gij2494312[sp]P70541[E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)]			synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331828, 29331827, 29331828, 264509, 265007, 265009, 264598, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486284, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)				UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]			UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]		Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264568

2246	94848710 (4491, 4492)	Novel Protein sim. GBank gi 4996096 dbj BAA78326.1 - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35698052, 264106, 264905, 264907, 265005, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 27486284, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gi 654065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52646365, 52645080, 35696052, 33656970, 52646317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486265, 18108387
2248	95412986 (4495, 4496)	Novel Protein sim. GBank gi 4758502 ref NP_004123.1 pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calthepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264689, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gi 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gi 3738140 emb CAA21241 - (AL031852) valyl-tRNA synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi 3218467 emb CAA07090.1 - (AJ006529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 284628, 55811576, 264555, 264556, 264557, 284558, 264559, 264588
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 284112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264488, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gil4502847 refNP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264569, 18108394, 18108398, 56182575, 56994075, 35698286, 22278999, 284094, 60432049, 264259, 29331822, 29331824, 28331825, 29331826, 60432288, 29331827, 29331828, 35696052, 264106, 264508, 264509, 264906, 264907, 29331830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433356, 60433438, 264758, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 21906765, 21906767, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263968, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35696423, 35695855, 264630, 264634, 264635, 264636, 264558, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264486, 264567, 18108391
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gil5541865 emb CAB51072.1 - (AL098858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264258, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264593, 264595, 21906754, 33109954, 87168474, 265011, 265017, 265019, 264682, 264764, 264369, 264288, 264766, 264685, 264686, 264768, 21906765, 21906766, 21906768, 21906769, 265020, 60170815, 52844150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gil3327174 dbj BAA31655 - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264768, 264688, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278998, 264681, 21906765, 21906766, 264567
2258	88090516 (4515, 4516)	Novel Protein sim. GBank gil3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1 - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108396, 65274572, 56182575, 22278997, 22278998, 284259, 29331822, 29331827, 264905, 66712502, 284908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 56181562, 265021, 60170615, 264890, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 264908, 35696423, 284511, 264635, 55812038, 264758, 265018, 265019, 264605, 284760, 264583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138 - (AL021306) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gi 4677759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278998, 29331822, 29331825, 60432289, 29331827, 35696052, 264508, 66712502, 52644045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21908767, 55811957, 35695917, 52844150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108381, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264908, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264486, 264766
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	8773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22278000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gij3560229[emb]CAA20697.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 35696052, 29331828, 264905, 264509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52844229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87168518, 264568, 264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2268	85693867 (4535, 4536)	Novel Protein sim. GBank gij728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII		cadherin	
2269	88177877 (4537, 4538)	Novel Protein sim. GBank gij103418[pr]S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113, 264763
2270	80410327 (4539, 4540)				
2271	91010392 (4541, 4542)			cyto450	264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)			UNCLASSIFIED	264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gij4176370 (AC005058) - similar to calcium-independent phospholipase A2: similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264689, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gij1480112[emb]CAA67961] - (X99642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21906765, 21906766, 21906767, 21906768, 52644150, 264693, 18108364, 35695763, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gij3165406 (AC004755) - fos37502_2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)			UNCLASSIFIED	264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	- glycoprotein	22278999, 35696052, 265008, 265019, 264369, 265020, 265022, 55810784, 264404, 22279002
2278	94133078 (4555, 4556)	Novel Protein sim. GBank gi 2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 265018, 33657023, 264639, 83373044, 284565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)	Novel Protein sim. GBank gi 4240289 dbj BAA74928.1 - (AB020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	- transport	265008, 33109954, 285010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264908, 264909, 52644045, 265008, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264686, 21908765, 21908767, 21906768, 21906769, 60170615, 264690, 52644150, 18108382, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U53840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21906767, 21906769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi 2495729 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810784, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4567, 4588)	Novel Protein sim. GBank gi 2498797 sp Q64311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424178, 52644507, 18108394, 52646842, 22278994, 35696286, 22278996, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87168559, 265018, 265018, 55811150, 264682, 264389, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33857182, 27486262, 27486264, 27486265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 264482, 264584 35695052, 264905, 264907, 264808, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264763, 264685, 264766, 264688, 264768, 264693, 264629, 35695855, 264631, 264634 35696286, 56182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264692, 55811576, 264555, 264557 264682
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gi 3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]	collagen		
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]	kinase		
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi 630905 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	UNCLASSIFIED	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	tm7		22278995, 56994075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	kinase		
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00400) - WD domain, G-beta repeat	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]	strucd		18108394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	84328834 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181562, 264769, 21908765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22279000, 264567
2283	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	- sinud	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2284	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	- nuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264888, 21908765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657108, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2285	85312200 (4589, 4590)			UNCLASSIFIED	22278998, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)				263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 dbj BAA83034.1 - (AB029005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4598)	Novel Protein sim. GBank gj3875051[embjCAB02849] - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424178, 56181686, 22278995, 35696286, 22278998, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 60424268, 35696052, 29331828, 66712502, 56182435, 264510, 265006, 60433438, 21806754, 33109954, 55811386, 285010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21906768, 21806767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108384, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35698423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22279000, 264482, 264567, 264486
2299	80193720 (4597, 4598)			UNCLASSIFIED	264369
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gj2443886 (AC002284) - Unknown protein [Arabidopsis thaliana]			264488, 22278996, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 285008, 284910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21908766, 21908767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22279002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gj2143637[pirj184505 - calcium-dependent actin-binding protein - rat]		struct	264908, 264758, 265017, 21906765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gj2887497 (AC004144) - R34001_1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gj4884194[embjCAB43220.1] - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gj2494182[spjQ10005]YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657349
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gj4972686[gbjAAD34738.1] - (AF132150) unknown [Drosophila melanogaster]			55274572, 22278996, 264908, 265006, 21906768, 264681, 264486

2306	85334940 (4611, 4612)	Novel Protein sim. GBank gi 4929565 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278985, 22278986, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 284508, 264905, 264907, 29331830, 264908, 284909, 264510, 265008, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 284601, 265017, 285018, 264604, 265019, 18108351, 264448, 264288, 264766, 264769, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35686423, 35695855, 264630, 264634, 264635, 264636, 284637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264488 264828
2307	78415283 (4613, 4614)			UNCLASSIFIED	
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278998, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 66712502, 60432228, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21908768, 265020, 284691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)			UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir 48281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	transcriptfactor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264883, 264288, 264369, 264688, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264486

2312	87549681 (4623, 4624)	Novel Protein sim. GBank gi 2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264258, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 27486261, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gi 3043626 dbj BAA25477 - (AB011123) KIAA0551 protein [Homo sapiens]			263981
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gi 5596714 emb CAB51401.1 - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2315	80430118 (4629, 4630)			UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gi 5531827 gb AAD44488.1 - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain		52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 285018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gi 5262613 emb CAB45746.1 - (AL080155) hypothetical protein [Homo sapiens]			264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 58994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21906754, 52644288, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 284448, 18108354, 264288, 264369, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4638, 4640)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase		22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21906765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi 3873837 emb CAB02700 - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...	UNCLASSIFIED		264488, 264687, 18108394, 264689, 21906765, 18108397, 18108398, 21906767, 21906768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170615, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gi 5678957 emb CAB51885.1 - (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	84840445 (4645, 4646)	Novel Protein sim. GBank gil2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - DnaJ domain	eph	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33856970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gil5419865 emb CAB46377.1 - (AL096732) hypothetical protein [Homo sapiens]		ATPase_associated	265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gil231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00067) - Cytochrome P450	Cyto450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gil231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)		UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gil4240227 dbj BAA74892.1 - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264768, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264539, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gil1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]		UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gil1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	UNCLASSIFIED	265017, 264685, 60432113, 264088
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gil5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009
2331	86990463 (4661, 4662)	Novel Protein sim. GBank gil2104452 emb CAB08779 - (Z95397) unknown [Schizosaccharomyces pombe]		ATPase_associated	35696286, 22278998, 29331824, 60424269, 265006, 265008, 265018, 264448, 264764, 21906765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gil3879985 emb CAA92691.1 - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C09493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...		UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gil4966270 gb AAB52261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gil4966270 gb AAB52261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gi 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi 1929056[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopodium obscurum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi 4495063[emb]CAB39181.1] - (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811388, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi 2224689[db]BAA20829] - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264908, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi 3873550[emb]CAA22127] - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	90937716 (4679, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264766, 264685, 21908769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	8775281 (4681, 4682)	Novel Protein sim. GBank gi 3874563[emb]CAB02797] - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264809, 264682, 22279000, 264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264584, 264565, 264566, 264567, 264907, 264512, 265011, 264683
2343	8775448 (4685, 4686)	Novel Protein sim. GBank gi 4929741[gb]AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	
2344	79953198 (4687, 4688)			UNCLASSIFIED	264758
2345	94319799 (4689, 4690)	Novel Protein sim. GBank gi 2506307[sp]P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	collagen	264488, 264259, 66712502, 264759, 83373044, 264566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gij1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87168559, 264603, 265019, 18108351, 264681, 264685, 21906768, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22278000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264694, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95186133 (4695, 4696)	Novel Protein sim. GBank gij1929056[lemb][CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35698423, 284631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gij4884106[lemb][CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35696052, 29146499, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906768, 21906767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gij728832[sp]P39189[ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!]		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gij731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gij1346955[sp]P48809[R827_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gij731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gi 4938503 emb CA843861.1 - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265006, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263967, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gi 5138920 gb AAD40377.1 - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109854, 21906764, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 33657109, 27486264, 35695763, 55810764, 18108379, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gi 4929741 gb AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gi 4218005 (AC006135) - putative viciin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gi 1086830 (U41264) - coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gi 3881545 emb CAA93779 - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	84232181 (4721, 4722)	Novel Protein sim. GBank gi 746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gij1171093 sp P19706 MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278999, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gij854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gij5639830 gb AAD45886.1 AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 35696286, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264908, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gij1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278998, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gij1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810764, 65274791, 264567
2368	94322190 (4735, 4736)				264628

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901 dbj BAA82158.1 - (AB0293343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644298, 52644228, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263987, 33657109, 27486285, 35695763, 18108370, 263974, 18108374, 18108378, 52644332, 263981, 18108385, 264508, 264909, 264596, 264369
2370	79804120 (4739, 4740)			UNCLASSIFIED	
2371	57280406 (4741, 4742)			UNCLASSIFIED	
2372	87642413 (4743, 4744)			UNCLASSIFIED	
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4589582 dbj BAA76813.1 - (AB023186) KIAA0969 protein [Homo sapiens]		UNCLASSIFIED	263967, 263981
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij5105131 dbj BAA80445.1 - (AF000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exonuclease family	UNCLASSIFIED	264634, 60432113
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115 sp P47758 SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264565
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	60432049, 29331824, 264907, 52644045, 264512, 60433358, 21906754, 52644288, 87168559, 264448, 21908765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005 gb AAD41239.1 - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	18108394, 55274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 33657023, 33657109, 18108370, 18108374, 18108378, 35696423, 264556, 83373044, 18108385, 18108388, 56526486, 22278000, 22279002, 264563
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482

2380	88923062 (4759, 4760)	Novel Protein sim. GBank gi 4502939 ref NP_001845.1 pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CAB36555 - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization Modifier domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811576, 284636, 264567
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276 - (AF119716) dMI-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432289, 264905, 264596, 21906754, 264769, 265022, 264693, 263967, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 db BAA19005 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	struct	264488, 52644507, 52645156, 52646365, 35696286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)			UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278998, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi 4929699 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906768, 21906767, 21906769, 29148629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14987890 (4773, 4774)				UNCLASSIFIED	264634
2388	11424604 (4775, 4776)				UNCLASSIFIED	264595
2389	85310650 (4777, 4778)	Novel Protein sim. GBank gil4758058[ref]NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor		dna_rna_bind	284488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 264511, 264512, 264910, 264591, 21906754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35698423, 264635, 264638, 264555, 83373044, 22279000, 264486
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gil1644239[dbj]BAA12223 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A		polymerase	52644507, 56182575, 22278995, 35698286, 22278996, 22278997, 22278999, 29331822, 29331825, 29331826, 35698052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35698423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56526486
2391	80036194 (4781, 4782)				UNCLASSIFIED	263976
2392	84245016 (4783, 4784)	Novel Protein sim. GBank gil4240169[dbj]BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat		nuclease	35696286, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35698423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi 4506667 ref NP_000993.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	- ribosomalprot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 58994075, 35696286, 22278996, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264909, 56182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264768, 264686, 264687, 264688, 264689, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264566, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AAD47636.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_ma_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264566

2398	95096700 (4791, 4792)	Novel Protein sim. GBank gij106322[pir][B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52645365, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21906766, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35698423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644298, 264803, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gij3258609 (AC005176) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gij786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gij2352822[gblAAB69285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1 - (AF008845) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644228, 264688, 21908764, 21908765, 52646365, 52646842, 21908766, 21908767, 21908768, 22278995, 35695917, 56994075, 35696288, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 8 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gi 4929575 gb AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gi 2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21908769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gi 464178 dbj BAA03581 - (D14853) polyprotein [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21908754, 265017, 265018, 265019, 264763, 264369, 21908765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gi 2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465005 (4813, 4814)			UNCLASSIFIED	264685, 264686
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gi 423442 pir S33513 - gene Fil protein - mouse		UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gij1176601[sp P45966 YNZ6_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264087, 29331822, 29331824, 29331827, 29148498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4818, 4820)	Novel Protein sim. GBank gij4966262[gb AAC48052.2] - (U64849) Contains similarity to Pfam domain: PF00646 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gij3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264368, 33657109, 58182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gij5410336[gb AAD43038.1] - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gij5262705[emb CAB45778.1] - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264805, 264509, 264908, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264689, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264584, 264585, 264586, 284587, 264486
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gij1082340[pir S52863 - DNA- binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433358, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 284558, 58182323, 83373044, 18108385, 87168518, 22279002

2415	88080002 (4828, 4830)	Novel Protein sim. GBank gij423915 pir A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432288, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264568
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284006 pir S18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264558, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)			UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432048, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077932 dbj BAA19879 - (D86556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AAB53003.1 - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87622683 (4853, 4854)	Novel Protein sim. GBank gil4680695[gb]/AAD27737.1[AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomal prot	264258, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21906766, 264691, 284692, 18108374, 18108377, 284557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gil1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278999, 35696052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22278002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gil601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 28331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)			UNCLASSIFIED	264112, 264631
2431	87649884 (4861, 4862)	Novel Protein sim. GBank gil3860729[emb]CAA14630] - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		29331826, 29331827, 35696052, 29146489, 264905, 264906, 264681, 264288, 264689, 21908765, 264692, 35698423
2432	80830333 (4863, 4864)	Novel Protein sim. GBank gil3876367[emb]CAA93287] - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gil2224593[dbj]BAA20784] - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264569, 264905, 265018, 264762, 264683, 264691, 264558, 264557, 264639, 264558
2434	19520148 (4867, 4868)				264563
2435	20759044 (4869, 4870)			UNCLASSIFIED	264555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gil1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gil3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2438	84143473 (4875, 4876)	Novel Protein sim. GBank gil3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264568, 264567

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gij4263519[gb]AAD15345] - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35698286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35898052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22279000, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 58182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gij3024889[sp]P56524[Y288 HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)]		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gij4506013[ref]NP_002703.1[pPPP1 - protein phosphatase 1, regulatory subunit 7]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gij1170658[sp]Q02975[KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gij4758824[ref]NP_004280.1[pNRF3 - nuclear factor (erythroid-derived 2)-like 3]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gij2135950[pir][S58222 - PQ-rich protein - human]			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gij4753887[emb]CAA05409.2] - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gij4885613[ref]NP_005409.1[pST5] - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)				UNCLASSIFIED	22278996, 22278997, 22278999, 29331826, 35696052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII			cadherin	264259, 264828, 265007, 264595, 265021, 56528486
2450	86597784 (4899, 4900)				UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gi 1710021 sp P35290 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family		glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35696052, 264907, 66712502, 29331830, 264910, 265009, 284758, 265017, 265018, 264762, 264448, 284288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gi 1504034 dbj BAA13216 - (D86980) KIAA0227 [Homo sapiens]			isomerase	264102, 264112, 264888, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat		ngfirecap	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gi 1076802 pir S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor		UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 284512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 284603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264688, 264768, 264769, 264534, 264691, 264692, 33657023, 284693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264486
2455	95288301 (4809, 4910)	Novel Protein sim. GBank gi 543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP.1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family		glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 284764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gi 2588630 (AC003079) - Ankryrin- like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat		kinase	264693

2457	84118375 (4913, 4914)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	556181686, 264805, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gij2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gij5441942 [gb]AAD43187.1 [AC004997] supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gij4929701 [gb]AAD34111.1 [AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	55274572, 35686286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29146499, 284102, 264109, 60433438, 265017, 285018, 265019, 264288, 21908765, 21906766, 21906769, 35695917, 265020, 284691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gij4426962 [gb]AAD20633 [AF126062] Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86998002 (4923, 4924)	Novel Protein sim. GBank gij5420387 [emb] [CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264909, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gij5052516 [gb]AAD38588.1 [AF14561 - (AF145613) BcDNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gij5410300 [gb]AAD43021.1 [AF100757] COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 285017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	85357483 (4928, 4930)	Novel Protein sim. GBank gi 4508401 ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - oncogene Eukaryotic protein kinase domain	18108392, 52644507, 52645158, 52846365, 22278994, 22278995, 35696288, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264767, 21908785, 21908767, 21908768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264389
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1 - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005595) - F16801_1, partial CDS [Homo sapiens]	UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pir J158106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat	29331824, 52644045, 265008, 264910, 265019, 21908785, 21906769, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 emb CAB46424.1 - (AL096749) DKFZp434G153 [Homo sapiens]	UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]	UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi 4539009 emb CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]		60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]		65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gi 1216486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - EGF-like domain	- Igi	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35696423, 83373044, 18108383, 18108385, 264584, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 284758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gi 1644232[dbj BAA11082] - (D67066) N-WASP [Bos taurus]		Im7	56994075, 22278999, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)			UNCLASSIFIED	264905, 284907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gi 5689469[dbj BAA83018.1] - (AB028989) KIAA1066 protein [Homo sapiens]		collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 284910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 284288, 264766, 264688, 284768, 21906788, 55811957, 265020, 264691, 264692, 264693, 264628, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gi 321249[pir S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 284768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gi 728831[sp P39188]ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!!		Kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gi 1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 284600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 284769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264108, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21906768, 21906767, 21906768, 21906789, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2588624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - !III ALU SUBFAMILY SB WARNING ENTRY !III		tm7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2483	85422415 (4985, 4986)	Novel Protein sim. GBank gi 4240307 dbj BAA74932.1 - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - R3H domain	struct	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264508, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 284600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21906765, 21906766, 21906767, 21906768, 21908769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 55274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2484	30783118 (4987, 4988)			UNCLASSIFIED	264907, 284601
2485	94234551 (4989, 4990)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		collagen	263994, 22278997, 35696052, 264509, 264905, 284906, 264907, 284908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264564, 264567, 264486
2486	80018765 (4991, 4992)	Novel Protein sim. GBank gi 4808220 emb CAB42832.1 - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]		struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2487	91723554 (4993, 4994)			UNCLASSIFIED	52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2488	87724633 (4995, 4996)	Novel Protein sim. GBank gi 1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED	29331827, 264512, 264910, 284288, 18108374, 35695855
2499	94685125 (4997, 4998)	Novel Protein sim. GBank gi 3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264908, 55812038, 264631, 264637, 264558

2500	94649324 (4999, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA21725 - (AL032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645156, 22278995, 56994075, 35696288, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 284448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gi 4929615 gb AAD34068.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35696286, 22278996, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2196874 emb CAA72638 - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gi 50420 emb CAA48220 - (X68101) trg [Rattus norvegicus]			284488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264906, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	9123328 (5011, 5012)	Novel Protein sim. GBank gi 2137562 pir 49635 - mouse Dhm1 protein - mouse		nuclease	284488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108378, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pK1AA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263994, 264592, 264595, 264369, 264686, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gi 4826433 emb CAB42889.1 - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gi 263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gi 3293537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278994, 22278986, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21908767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486262, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gi 4323152 gb AAD16228.1 - (AF098863) Ets-protein Spi-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gi 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 264763, 264683, 264768, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi 3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52845156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gi 3757727 emb CAA18783 - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gi 4220527 emb CAA23000 - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657108, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5038)	Novel Protein sim. GBank gil4928591 gb AAD34056.1 AF15181 - (AF151819) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433358, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gil4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4 (AC004883) similar to KIAA0766; similar to PID:g3882253 [Homo sapiens]		kinase	264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gil4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4		transport	264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gil5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263994, 65274572, 22278995, 22278998, 264259, 29331822, 29331825, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265006, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gil4580011 gb AAD24201.1 U81002_ - (U81002) TRAF4 associated factor 1 [Homo sapiens]		transport	264489, 22278997, 20281171, 21906754, 35695917, 263987, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gil1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21806765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486261, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gjl2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase: DGCN2 [Drosophila melanogaster]		Kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21908765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gjl4589628[dbj]BAA76836.1] - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21908768, 21908769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33857023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264288, 264486, 264567, 264766, 264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gjl2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	264908, 264769, 265020, 265021, 18108383
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gjl3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21906768, 33857023, 87168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gjl2864625[emb]CAA16972] - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gjl437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5068)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21908769, 265020, 265022, 33557109, 22279000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gij4468311[emb]CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gij728836[sp]P39193[ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!]		kinase	18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264789, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gij4557026[ref]NP_003913.1[pHERC - guanine nucleotide exchange factor p532]		ubiquitin	65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144816 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264766, 87168518, 22278000, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gij1362647[pir]SS3876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gij1711658[sp]P54797[T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION]		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gil5225320 gb AAD40850.1 AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646365, 52646842, 65274572, 22278994, 35898288, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35898052, 33656970, 284907, 264909, 52644045, 264510, 265008, 284512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644229, 284769, 21906768, 21906767, 21906769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gil5419857 emb CAB46374.1 - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331828, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 284689, 21906765, 21906767, 21906769, 80170815, 264692, 264693, 55811576, 65274791, 284636, 264558, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gil2498110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 284905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 284448, 264686, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742645 (5089, 5090)	Novel Protein sim. GBank gil3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170615, 264692, 33657109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gil2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143869 (5093, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34064.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56894075, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35695052, 29331828, 264104, 264508, 264905, 264806, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27488261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22279002, 264564, 264566, 264486
2548	88179079 (5095, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108388, 60431602, 18108376, 35696423, 56182323, 18108387, 264567
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir I52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gjl4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35698423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gjl711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 284602, 284910, 264634, 284760, 264555, 264762, 264806, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264766, 22278997, 29331822, 264508, 21908769, 33657023, 33657109, 56182323
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gjl728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY !!!		cadherin	
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gjl4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gjl4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567, 264595
2557	79437803 (5113, 5114)				
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gjl119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gjl4538998 emb CAB39619.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gjl5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein))) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gjl5326825 gb AAD42056.1 AF04495 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432228, 87168559, 265017, 265018, 265019, 264689, 21908766, 21908769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	5694075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170615, 33657023, 264693, 35695855, 87168518
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gi 4886447 emb CAB43371.1 - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52644045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352944 sp P47179 J9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfotransferase	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530806 (5129, 5130)			UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi 628012 pir A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	- struct	18108370, 35695855, 264556, 264558, 18108383
2567	86143590 (5133, 5134)				265020, 60170615
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gi 466009 sp P34548 YNU4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gij2599560 gb AAB84166.1 - (AF029674) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	18108394, 56182575, 56181686, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 284592, 60433356, 60433438, 21906754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20261069, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264566
2570	94136754 (5139, 5140)	Novel Protein sim. GBank gij4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gij732218 sp P34609 YO60 CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III	struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gij4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]	UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	85313928 (5145, 5146)	Novel Protein sim. GBank gil399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432228, 264593, 60433356, 264594, 60433438, 264585, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108388, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264584, 264585, 264586, 264587
2574	84746814 (5147, 5148)	Novel Protein sim. GBank gil3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gil4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gil4680681 gb AAD27730.1 AF13295 - (AF13295) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gil4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87766941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264768, 21908769, 264628, 264630, 264634, 264639, 264563
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88166788 (5159, 5160)	Novel Protein sim. GBank gi 2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]				265007, 265018, 264762
2581	87899048 (5161, 5162)	Novel Protein sim. GBank gi 4406642[gb]/AAD20049] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen		56994075, 29331824, 29331826, 29331828, 264905, 60433358, 60433438, 264758, 87168559, 21906769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi 2739387 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph		264488, 264907, 264908, 264910, 264784, 264684, 264766, 264838, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112[emb]/CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcriptfactor		56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264598, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED		264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi 2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase		264768
2586	91226136 (5171, 5172)					22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433358, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56528486, 22279002
2587	80430943 (5173, 5174)					264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED		264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 3021598[emb]/CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED		35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35696423, 264636
2590	87054528 (5179, 5180)	Novel Protein sim. GBank gi 2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase		22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi 5702202[gb]/AAD47199.1 AF12916 - (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph		264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi 3024998 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331828, 60432289, 29331827, 29331828, 264905, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		tm7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF151817) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264584, 264566, 264567
2595	79561676 (5189, 5190)			UNCLASSIFIED	264692
2596	87538637 (5191, 5192)	Novel Protein sim. GBank gi 4309681 gb AAD15478 - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2597	94784089 (5193, 5194)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 dbj BAA10838 - (D64006) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264565
2599	87642889 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF109719) - BAT2 [Mus musculus]		MHC	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264566
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33857109, 18108370, 18108376, 56182323, 18108381, 18108385, 22279002, 264563 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 406632 gb AAD20047 - (AF131801) Unknown [Homo sapiens]			264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35896052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gi 3122367 sp Q61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_006468.1 pRRP2 - RAS-related on chromosome 22		oncogene	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi 3628745 db BAA33366 - (AB013721) mitsugumin 23 (Oryctolagus cuniculus)		UNCLASSIFIED	
2606	87746406 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gi 4826626 gb AAD30202.1 - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264908, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264688, 21908765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	61734766 (5215, 5216)	Novel Protein sim. GBank gi 2226005 (U49973) - ORF2: function unknown [Homo sapiens]			
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21908765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2610	80177654 (5219, 5220)	Novel Protein sim. GBank gi 4336855 gb AAD17989 - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcription factor	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811578, 264638, 87168518, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gi 3876761 emb CAA92994 - (Z68760) predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278999, 265017, 264684, 21906768, 22279000
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gi 5533081 gb AAD45009.1 AF16118 - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52844229, 21908765, 33657109, 27486264, 18108370, 263972, 264555, 60432113
2615	87381986 (5229, 5230)			UNCLASSIFIED	264768, 18108394, 284692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gi 3876761 emb CAA92994 - (Z68760) predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278895, 22278997, 22278998, 60432048, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264567
2617	86976888 (5233, 5234)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gi 3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264906, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56528488, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank gi 2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	9531481 (5239, 5240)	Novel Protein sim. GBank gi 4322567 gb AAD16097 - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35696286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52844150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 264594, 264636
2621	80253495 (5241, 5242)				
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gi 4557341 ref NP_001174.1 pATP6 - ATPase, H ⁺ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			264488, 264906, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBank gi 3880355 emb CAB05299 - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gjl3880355[embjCAB05299] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35696052, 29146499, 66712502, 52644045, 265007, 265008, 60433356, 33109954, 21906754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gjl2887429[dbjBAA24857] - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gjl487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gjl88462[pir]A27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gjl3123552[embjCAA18609] - (AL022578) dJ993P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278997, 22278998, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21906765, 21906768, 265022, 65274791, 264638, 18108387, 87168518, 22278002
2629	87376480 (5257, 5258)	Novel Protein sim. GBank gjl4929595[gbjAAD34058.1]AF15182 - (AF151821) CGI-63 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	78188364 (5259, 5260)	Novel Protein sim. GBank gjl321605[pir]JQ1161 - Gag protein - Visna virus (strain EV1)		UNCLASSIFIED	264636, 18108385
2631	94845909 (5261, 5262)	Novel Protein sim. GBank gjl321605[pir]JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - dna_ma_bind Zinc finger, CCHC class		52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35698286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52844150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486
2632	36730414 (5263, 5264)				264585

2633	85011617 (5265, 5266)	Novel Protein sim. GBank gij1139548[dbj BAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265006, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811576, 264638, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264565
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gij5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gij4680663[gb AAD27721.1]AF13294 - (AF132946) CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695855, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3879146[emb CAB07646] - (Z93386) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	264569, 29331822, 29331828, 265006, 60170831, 264681, 264765, 264685, 29148627, 21906769, 29148784, 265022, 60170615, 264635, 18108385, 56526486, 22279002, 264567
2637	95011289 (5273, 5274)	Novel Protein sim. GBank gij4758208[ref NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278998, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170815, 264691, 33657023, 264692, 264693, 65274620, 27486284, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264486, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gi 4929689 gb AAD34105.1 AF15186 - (AF15188) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 58182575, 22278995, 22278996, 35696286, 22278997, 22278998, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 264905, 52644045, 56182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264769, 52644229, 56181562, 29148627, 29148629, 55811957, 29148764, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810764, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95361348 (5277, 5278)	Novel Protein sim. GBank gi 2190007 dbj BAA20355 - (AB004109) phosphatidylserine synthase II [Cricetulus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264563, 264584, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm. score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm. score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11669834 (5281, 5282)			UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22279002
2643	87643961 (5285, 5286)	Novel Protein sim. GBank gi 4490304 emb CAB38795.1 - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl_recpl	264107, 264687
2645	17277228 (5289, 5290)			UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	Novel Protein sim. GBank gi 1708722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 264632, 83373044

2647	91212978 (5283, 5284)				UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 28331825, 60424269, 60432289, 35696052, 68712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 265019, 264448, 264288, 56181562, 21908765, 21906766, 21906768, 21908769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)					29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gi 3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]			UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331828, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264686, 264688, 21906765, 21906768, 60170815, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264563, 264685
2650	87297533 (5299, 5300)	Novel Protein sim. GBank gi 5360271 dbj BAA81908.1 - (AB0293335) HrPET-3 [Halocynthia roretzi]				
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gi 4240225 dbj BAA74891.1 - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - synthase Laminin G domain			29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)	Novel Protein sim. GBank gi 4493956 emb CAB11123.2 - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....			UNCLASSIFIED	264692
2653	87798735 (5305, 5306)				UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)					60424179, 65274572, 56182575, 264259, 56182181, 284908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gi 3875272 emb CAB02861 - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcript factor		56182575, 56181886, 264092, 264259, 56182181, 60432289, 264807, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank gi 3043718 dbj BAA25523 - (AB011169) KIAA0597 protein [Homo sapiens]				264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gij5689509[dbj BAA83038.1] - (AB029009) KIAA1086 protein [Homo sapiens]			dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gij3688089 (AC005757) - R32611_1 [Homo sapiens]		Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331828, 29331828, 265019, 264883, 21906768, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gij728837[sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433358, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gij4758048[ref NP_004739.1 pCPR8 - cell cycle progression 8 protein			glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486262, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)					264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gij3874714[emb CAA91263] - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]			dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gij1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gij4884406[emb CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]			UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2666	87826472 (5331, 5332)	Novel Protein sim. GBank gij5106956[gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gij2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1		Contains protein domain (PF01138) - 3' exonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_006327.1 pZYG - ZYG homolog		UNCLASSIFIED	56181686, 35696286, 22278998, 22278998, 22278998, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264682, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pir JC4899 - proline rich protein - rat			264489, 264689, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331828, 29331827, 35696052, 29331828, 29146498, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10362 YD8B_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD29444.1 AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]		transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC006341) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gij5457337[embjCAB41505.2] - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00544) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gij4758824[refNP_004280.1]pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	94329600 (5353, 5354)	Novel Protein sim. GBank gij1079042[pirjIS52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264490, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52644045, 265006, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gij86760 pir A40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52646842, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109854, 52646317, 21906754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gij1709233 sp P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 284909, 56182435, 264513, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gij4589604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264259, 264102, 264905, 264908, 285007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	80933844 (5361, 5362)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gij423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 55526486
2683	8777405 (5365, 5366)	Novel Protein sim. GBank gij5114351 gb AAD40286.1 - (AF158271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264909, 264769, 264635, 264636

2684	85787151 (5367, 5366)	Novel Protein sim. GBank gij4886469[embjCAB43385.1] - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054299 (5369, 5370)	Novel Protein sim. GBank gij3342729 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED	
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gij4650844[dbjBAA77027.1] - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - struct Kelch motif		264259, 29331822, 604322289, 29331827, 29331830, 264909, 264512, 264596, 264769, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87998183 (5373, 5374)	Novel Protein sim. GBank gij5281314[gb AAD41475.1 AF133123] transcription factor [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108396, 22278996, 35696286, 22278997, 29331826, 29331828, 68712502, 21906754, 265011, 264760, 264761, 264763, 264689, 21906765, 35696423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gij3880023[embjCAA97339] - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264906, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906766, 21906768, 33657023, 33657182, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gij4107276[embjCAA67130] - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264566
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gij3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Protyl oligopeptidase family	peptidase	
2693	20438807 (5385, 5386)	Novel Protein sim. GBank gij3122400[sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264592
2694	94111918 (5387, 5388)				264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gij4972740[gb AAD34765.1] - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264566
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gij728831[sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		synthase	264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gi 5689473 dbj BAA83020.1 - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gi 841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcriptfactor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 28331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21908785, 21908766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gi 5174395 ref NP_006006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gi 1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645158, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146499, 265008, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21908768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gi 5689399 dbj BAA82983.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00842) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335694[gb AAB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29146499, 264905, 264908, 264907, 52644045, 264511, 33657402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij3255952[emb CAA16821.1] - (AL021728) /prediction=(method:: /match=(desc: [[Drosophila melanogaster]	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33656970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21906754, 52644296, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000, 22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417294 (AC004381) - Unknown gene product [Homo sapiens]			65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bs 147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein (human, brain, Peptide, 204 aa]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED		29331824, 264759, 264693, 18108382, 18108388
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gil3122400 sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264768, 21908764, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27466262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264764, 264568, 264288, 264766
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gil5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	264488, 35696286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264906, 66712502, 52644045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gil25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gil4321968 gb AAD15897 - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gil2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264553
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gil3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			264593, 264558
2718	78604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gil746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gij1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	18108374, 60424179, 264489, 56182435, 21906765, 21908768, 35696423, 22278997, 265020, 265022, 265008, 264092, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 60424269, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 68712502, 52644045, 264909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4929663 [gbjAAD34092.1] AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023	22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gij3212997 [gbjAAC23434.1] - (AC004997) match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040854 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - oncogene TBC domain	35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)		UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264766, 284687, 284629, 264636, 264486
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gij4680681 [gbjAAD27730.1] AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]	MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gil731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridyate synthase	synthase	55274572, 55182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264636, 55812323, 87168518, 60432113, 22279000, 264564, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gj 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811857, 35695855, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gj 2408095 emb CAB16300 - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	55274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gj 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56526486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gil723239 sp Q10166 YAU8_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265008, 264758, 264762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gj 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567
2733	87363060 (5465, 5466)			UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gj 451962 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcript factor	60424179, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433556, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5468, 5470)	Novel Protein sim. GBank gi 3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 29146498, 264108, 264909, 284112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gi 2558501 dbj BAA22896 - (D63850) hepatoma-derived growth factor [Mus musculus]			264488, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gi 3417386 emb CAA75495 - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696288, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 60432229, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gi 3242764 (AC005154) - similar to protein U28928 (PID:g881308) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170815, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gi 4758412 ref NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264369, 29148627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank gi 4468311 emb CAB37992 - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264906, 264908, 265006, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264369, 264288

2745	87740125 (5488, 5480)	Novel Protein sim. GBank gi 4405795 gb AAD19826 - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264758, 264601, 265017, 264604, 264763, 264288, 264686, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gi 4758738 ref NP_004680.1 pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 265006, 60170831, 264596, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gi 4557803 ref NP_000262.1 pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264686, 264768, 21906769, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35696423, 35695855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gi 4191272 emb CAA09984 - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56526486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gi 1872498 (U74297) - PiUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gi 3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5506)	Novel Protein sim. GBank gj351648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 264288, 56181562, 21906767, 21906768, 265021, 264693, 18108374, 65274791, 264632, 56182323, 22279002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gj535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35696052, 29331828, 264906, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21906765, 21906767, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5509, 5510)	Novel Protein sim. GBank gj2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00095) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)			UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gj1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	eph	85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gj3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank gj2072200 (U94863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 284508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gj4914573[emb]CAB43685.1 - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	nuclease	22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21906768, 21906769, 265020, 56182323, 22279002, 264563
2762	87592599 (5523, 5524)	Novel Protein sim. GBank gj3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264906, 264909, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2763	87539968 (5525, 5526)	Novel Protein sim. GBank gj3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264368, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gj2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27486282, 56182323, 56526486, 87168518, 264487

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gi 4688672 emb CAA17688.2 - (AL022018) /prediction=(method:: /prediction=(method:: /match=(desc: [Drosophila melanogaster]			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168559, 264600, 285018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35698423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gi 5441611 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 80433356, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gi 1079451 pir A55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gi 5441322 emb CAB46721.1 - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35698052, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264488, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gij5419859[embjCAB46375.1] - (AL098725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 284369, 284288, 60170615, 264691, 33657023, 264682, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 284629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gij5701865[embjCAB52157.1] - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 284629, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gij3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264369
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gij4885531[re NP_005465.1 pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264768, 21906769, 33657109, 263978, 284555, 264638, 264557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gij3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263976, 56182435, 264689, 55810764, 21906766, 35696423, 55811576, 65274791, 56181686, 55811957, 35695855, 284110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27486261, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264766, 263974
2774	67819908 (5547, 5548)	Novel Protein sim. GBank gij465852[sp P34388 YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35698423, 35695855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4689132 gb AAD2775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7/pS5e	ribosomal prot	264488, 22278995, 56994075, 22278998, 3569288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264582, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 58182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2776	87791557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35896052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pHKGK] - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 469352 gb AAD21222] - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN] - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278996, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5566)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII			Im7	264909, 264628, 263978, 263981
2784	87614360 (5567, 5568)					264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pir J58890 - collapsin response mediator protein - human			UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 21906769, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase: DGCN2 [Drosophila melanogaster]		Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen			UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170615, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 2279002, 55811150, 264369, 264288
2788	88080644 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]			UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2495729 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)			UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1 - (AJ242978) p621 [Homo sapiens]			strut	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]				21906764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1 - (AF045642) No definition line found [Caenorhabditis elegans]				22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264906, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264766, 52644229, 21906765, 21906766, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 264636, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)				UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)				UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi 5454146 ref NP_008348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35896286, 22278988, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331828, 29331827, 35698052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906768, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264587
2786	94648857 (5591, 5592)	Novel Protein sim. GBank gi 4680651 gb AAD27715.1 AF13294 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 284908, 66712502, 56182435, 264510, 265008, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264596, 21908754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 284448, 264682, 264369, 264288, 264585, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2787	95110790 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29148499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265018, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 285020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2788	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35696052, 29331828, 264809, 60433356, 33657402, 33109954, 87168474, 264448, 52644229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74929.1] - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	284488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264686, 60170815, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264584, 264586, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC00658 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	264639
2804	57111131 (5607, 5608)			peptidase	264566
2805	87398486 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gjl4468310[embjCAB37991] - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433358, 264594, 60433438, 52646317, 21908754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gjl5541863[embjCAB51071.1] - (AL096857) hypothetical protein [Homo sapiens]	MHC	UNCLASSIFIED	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gjl2772561 (AC004002) - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:g118965) [Homo sapiens]	ATPase_associated	UNCLASSIFIED	18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29148629, 29148784, 264693
2811	91235845 (5621, 5622)	Novel Protein sim. GBank gjl3264583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1828773) [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)			UNCLASSIFIED	264106
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gjl4240273[dbjBAA74915.1] - (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gjl3548791 (AC005620) - R33590_1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	65274572
2815	79774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)	Novel Protein sim. GBank gjl5420389[embjCAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 284910, 265011, 264760, 264681, 264766, 264769, 284689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi 1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263978, 264634, 264636, 264639, 264564, 264565, 264566, 264488, 264587
2818	88073579 (5635, 5638)	Novel Protein sim. GBank gi 549986 (U13149) - possible apospory-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gi 4929773 gb AAD34147.1 AF152097 - (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264636
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi 222467 dbj BAA20820 - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906765, 60170615, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi 3559683 emb CAA22020 - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gil398144 splP02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 285006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91229615 (5655, 5656)	Novel Protein sim. GBank gil3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	29331822, 35698052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35696423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gil4680689 gb AAD27734.1 AF13295 - (AF132959) CGI-25 protein [Homo sapiens]		22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486 265008, 265019, 264639, 22279002
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gil2498667 splQ61200 NPH1_MOUSE - NEUREXOPHILIN 1		
2831	87614717 (5661, 5662)		UNCLASSIFIED	265017
2832	87631809 (5663, 5664)		UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gil5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gil2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]		263972
2835	8775712 (5669, 5670)	Novel Protein sim. GBank gil4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]	ATPase_associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gil2351568 (U76618) - N-RAP [Mus musculus]	transcription factor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)			UNCLASSIFIED	264555
2840	87774665 (5679, 5680)	Novel Protein sim. GBank gij1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj BAA20790] - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)				264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij5578957[embjCAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp Q08878 FBLC_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox		29146498, 87168474, 264686, 35696423, 83373044, 264564
2846	86318613 (5691, 5692)	Novel Protein sim. GBank gij5306263[gb AAD41995.1 AC006233] unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264558
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij3399676 (AC005390) - R31180_1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij5262615[embjCAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)			UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321619[gb]AAD15788.1] - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695855, 284556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - WW domain	kinase	56182575, 55811150, 264690, 27486262, 27486265, 264632, 56182323, 56526488, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	dna_rna_bind	35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040[dbj]BAA13219] - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486262, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	struct	22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585[sp]P35227[ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	dna_rna_bind	264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52844045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264564, 264566, 264486, 264567
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gij4325320[gb]AAD17331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532599 (5718, 5720)	Novel Protein sim. GBank gi 4469186 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264510, 264511, 33109954, 18108351, 264683, 264765, 264389, 264686, 21906765, 264691, 264692, 264693, 18108388, 22279002, 264482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi 3941730 (AF108083) - BS4 [Homo sapiens]			264369, 264692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN] - leucine-rich neuronal protein		UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi 3249088 (AC004473) - Contains similarity to golgiath protein gb M97204 from D. melanogster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	56994075, 35686286, 22278998, 29331822, 29331824, 35696052, 29331828, 264106, 264511, 55812038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657349, 264629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi 1079451 pir JA55463 - Tropomodulin, skeletal muscle - chicken		struct	264259, 264910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gi 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gi 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN		glycoprotein	65274572, 22278996, 22278998, 22278999, 264259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 264448, 264764, 52644150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264488, 264768, 21906768, 22278998, 265022, 264259, 264508, 264905, 264907, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264563, 264088, 264566, 264764, 264369, 264567, 264486, 264288, 264766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gi 1292868 emb CAA63923 - (X94232) t-Cell activation protein [Homo sapiens]			18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52844045, 264828, 265008, 265007, 265008, 265009, 264591, 60432229, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108388, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)			UNCLASSIFIED	264369
2870	84404574 (5739, 5740)			UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gi 112205 pir B39066 - proline-rich protein 15 - rat		kinase	263981
2873	88094252 (5745, 5746)			UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313549 (5747, 5748)	Novel Protein sim. GBank gjl3212854 (AC004005) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56984075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33655970, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gjl2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 29146499, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gjl2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Igf		
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gjl4704208[emb]CAB41646.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]			52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21908766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gjl3876775[emb]CAB03067] - (Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - Uncharacterized protein family UPF0034	UNCLASSIFIED	264488, 264239, 29331822, 29331826, 264905, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2878	87868122 (5757, 5758)	Novel Protein sim. GBank gi 4895145 gb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi 4680703 gb AAD2774.1 (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi 733571 (U23452) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi 118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi 4868008 gb AAD31087.1 (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)				265018, 264634
2885	83006306 (5769, 5770)	Novel Protein sim. GBank gi 2224697 dbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	- complementrecept	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- transcriptfactor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gij854065jembjCAA58337j - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264766
2881	88094428 (5781, 5782)	Novel Protein sim. GBank gij387775jembjCAB01508j - (Z78064) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66026 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95418745 (5783, 5784)	Novel Protein sim. GBank gij4929759jgbjAAD34140.1jAF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gij5669015jgbjAAD46135.1j - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor		264259, 265006, 60433438, 52644296, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gij3924708jembjCAA84646j - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gij4885549jrefjNP_005456.1jppKBG - protein kinase B gamma	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 264906, 284908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gij4502877jrefjNP_001296.1jppCLDN - Clostridium perfringens enterotoxin receptor 1		UNCLASSIFIED		60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 284629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)			UNCLASSIFIED		22278995, 264604, 18108385, 264566

2899	80357670 (5797, 5798)	Novel Protein sim. GBank gij4581470[emb]CAB40137.1] - (Y18483) SLC7A8 protein [Homo sapiens]		UNCLASSIFIED	264764, 21906764, 264692
2900	94233538 (5799, 5800)			glycoprotein	65274572, 56182575, 35696286, 60432049, 284259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gij4759272[ref]NP_004614.1pTTC4 - tetrairicopeptide repeat domain 4		phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gij2414615[emb]CAB16364] - (Z99259) hypothetical protein [Schizosaccharomyces pombe]			284683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gij1079318[pr]IS52241 - XLCL2 protein - African clawed frog			264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86456072 (5807, 5808)	Novel Protein sim. GBank gij5639823[gb]AAD45885.1[AF14367] - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]		UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gij728837[sp]P39194[ALU7_HUMAN - III] ALU SUBFAMILY SQ WARNING ENTRY III]		oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gij4689256[gb]AAD27831.1[AF12185] - (AF121858) sorting nexin 8 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264586

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - eph DnaJ domain	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 284595, 55812038, 21906754, 55811386, 265019, 284682, 264369, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2809	87420225 (5817, 5818)		eph	264259, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi 4539335 emb CAB37483.1 - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4469187 emb CAB38415.1 - (AL031588) dJ116331.3 (novel protein similar to mouse B99) [Homo sapiens]	glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637 gb AAD34079.1 AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED Zinc finger, C2H2 type	52644507, 52645156, 52846842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)			264557

2915	88031972 (5828, 5830)	Novel Protein sim. GBank gil5174485 ref NP_06030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - lph Lectin C-type domain	264569, 264488, 264687, 264768, 21906768, 52646842, 21906767, 21906768, 56182575, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 284259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264908, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264766
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gil510485 dbj BAA80165.1 - (AP000061) 305aa long hypothetical dTDP-4- dehydrothamnose reductase [Aeropyrum pernix]	dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gil3169065 emb CAA19260.1 - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gil539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gil2564955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486284, 27486265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gij4580013 gb AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35686052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433355, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56526486, 87168518, 22279000, 22279002
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gij4589514 dbj BAA76779.1 - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264906, 264909, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29148627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264488
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gij4835268 emb CAB42898.2 - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108378, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264568
2924	87791967 (5847, 5848)	Novel Protein sim. GBank gij2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	265017, 264628, 20281152, 264556
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gij2388986 emb CAB11718 - (Z98980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2926	95343003 (5851, 5852)					29331828, 265011, 264768, 264689
2927	80408018 (5853, 5854)	Novel Protein sim. GBank gi 283032 pir S22456 - hydroxyproline-rich glycoprotein - perennial leosinte				264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)				UNCLASSIFIED	264559
2929	81622820 (5857, 5858)	Novel Protein sim. GBank gi 3413320 emb CAA06915 - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]			UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 265009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33857109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)				UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33		UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906768, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264566
2932	79632623 (5863, 5864)					264906, 264907
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gi 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase			264488, 18108392, 56182375, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486262, 264628, 87168518, 22279000
2935	86410579 (5868, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21906754, 265018, 265019, 264448, 264769, 21906764, 21906765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi 5174409[refNP_006101.1]pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21906765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567, 264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433438, 55812038, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 60170615, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22279002
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi 3319990[emb CAA76720] - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi 3979900[emb CAA99909] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	

2940	95011103 (5879, 5880)				UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264784, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dbj BAA32300 - (AB007924) KIAA0455 protein [Homo sapiens]			UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25			glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]			collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 284593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1 - (AL049660) 1-acylceroi-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		ATPase_associated	56994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56528486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	Contains protein domain (PF00096) - Zinc finger, C2H2 type		UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264908, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264389, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264806, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264638, 264637, 18108380, 264638, 264639, 83373044, 264565, 264566, 264486, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF056116) Ali-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432228, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir [S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)]		UNCLASSIFIED	22278996, 22278997, 60432228, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52644229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 35696423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 YOJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264556, 56526486, 264486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264693

2852	95329952 (5903, 5904)	Novel Protein sim. GBank gi 5596693 emb CAB51405.1 - (AL096881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.		264687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433358, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2853	88093575 (5905, 5906)	Novel Protein sim. GBank gi 119522 sp P10658 SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108396, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52646317, 21906754, 33657084, 52644296, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108384, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2854	88086288 (5907, 5908)	Novel Protein sim. GBank gi 4885261 ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	tgf	
2855	87698426 (5909, 5910)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21906769, 265021, 60170615, 55810764, 264567
2856	85789745 (5911, 5912)	Novel Protein sim. GBank gi 4689254 gb AAD27830.1 AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21906768
2857	90933301 (5913, 5914)	Novel Protein sim. GBank gi 4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2858	87440014 (5915, 5916)	Novel Protein sim. GBank gi 4240257 db BAA74907.1 - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 284631, 284567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gi 988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene	263994, 22278997, 264259, 60432049, 29331826, 29331828, 35896052, 29331830, 66712502, 58182435, 265006, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264768, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486285, 18108374, 65274791, 35695855, 83373044, 56526486, 60432113
2860	87420091 (5919, 5920)			UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2861	95413416 (5921, 5922)	Novel Protein sim. GBank gi 5596646 emb CA805177.2 - (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52844045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2862	87912700 (5923, 5924)			UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52846317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2863	95313464 (5925, 5926)	Novel Protein sim. GBank gi 4240223 dbj BAA74890.1 - (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 284693, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	94324617 (5927, 5928)			UNCLASSIFIED	264259, 29331826, 33657402, 265017, 265018, 264692, 18108368, 35698423, 83373044, 18108388

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRML - Kreisler (mouse) maf- related leucine zipper homolog		transcriptfactor	264259, 29331826, 264508, 264509, 264805, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264567, 18108391 60432289, 264682, 264448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264488
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		264687, 52645156, 21906765, 52646365, 21906767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264638, 264690, 52644150, 264259, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22279000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 66712502, 264566, 264369, 264288
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SUI.S7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264359, 52644229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2970	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gij728837[sp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII]		Im7	264488, 56182575, 35686286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 284910, 21908754, 87168559, 265018, 265019, 18108351, 264689, 21906765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 284567
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gij728836[sp]P39193[ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII]	kinase		265017, 35695917, 265021, 33657109, 22279002, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gjj2746789 (AF040642) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED		29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gjj786117 (L41834) - nuclear protein [Ensis minor]	UNCLASSIFIED		18108392, 52644507, 56182575, 56181686, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21906754, 55811386, 52644286, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gjj3880812[emb]CAA19508] - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gij5679136[g]AAD46874.1[AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278996, 264908, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gjj5262751[emb]CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2978	87332059 (5955, 5956)	Novel Protein sim. GBank gi 746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2979	91725256 (5957, 5958)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		complement	264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2980	86296600 (5959, 5960)				265009, 21906767, 263981, 22279000
2981	87376330 (5961, 5962)			UNCLASSIFIED	264629, 264564
2982	95303675 (5963, 5964)	Novel Protein sim. GBank gi 4929767 gb AAD34144.1 AF15190 - (AF151907) CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2983	91725258 (5965, 5966)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2984	94136467 (5967, 5968)	Novel Protein sim. GBank gi 2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (P D:g1130619) [Homo sapiens]		ATPase_associated	
2985	87099072 (5969, 5970)	Novel Protein sim. GBank gi 103160 pir S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2986	86284861 (5971, 5972)				55811957, 264566
2987	86455934 (5973, 5974)			UNCLASSIFIED	264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4679028 gb AAD27002.1 - (AF077207) HSPC021 (Homo sapiens)		UNCLASSIFIED	264488, 65274572, 22278995, 22278998, 22278997, 22278999, 284092, 264094, 264259, 60432049, 29331824, 29331828, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433358, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264389, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113671 sp P23964 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII		kinase	22278996, 22278997, 284905, 264511, 60170831, 264593, 265019, 21908765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gi 2829836 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	oncogene	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)			UNCLASSIFIED	264563
2992	85425164 (5983, 5984)			UNCLASSIFIED	264259, 265019, 264689, 18108385
2993	94325363 (5985, 5986)			UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2496549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02		transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264566, 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]			
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	65274572, 35696286, 264259, 29331824, 35696052, 29146499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gij4589652[dj]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331826, 35996052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 52646365, 22278997, 264508, 264908, 18108351, 21908765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gij3947589[emb]CAA22252] - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 28147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gij115408[sp]P18835[CC]19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264596, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486281, 264628, 264629, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gij1163174 (U32575) - similar to yeast Sec6p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264564
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gij2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g70911) [Homo sapiens]		calthepsin	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gij3599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]		UNCLASSIFIED	

3003	86848079 (6005, 6006)	Novel Protein sim. GBank gi 1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gi 2224629[dbj BAA20802] - (AB002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 264601, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gi 4680659[gb AAD27719.1 AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gi 3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gi 2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gi 3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	52646842, 56182575, 22278995, 22278996, 284259, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 284600, 265017, 265018, 265019, 284760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 58182323, 264559, 18108385, 18108388, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gi 4927370[gb AAD33084.1 AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gi 5052318[gb AAD38501.1 AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank gi 3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35698286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811578, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gi 3878374[emb]CAA93081] - (Z68879) Similarity to Yeast Chi12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	264760
3015	86995466 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gi 168819[sp]P41733[CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gi 4589658[dbj]BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21908769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558
3019	94148231 (6037, 6038)	Novel Protein sim. GBank gi 3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264569, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 67168518, 22279000, 22279002, 264563
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gi 3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gi 3880889[emb CAB09005] - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 293331826, 29331828, 264288, 264566
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gi 416592[sp P32323JAG1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906769, 55811957, 35695917, 264690, 264555, 264559
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811576

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gi 3024052 sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263967, 20281149, 20281069, 263975, 263977, 20281071, 56528486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gi 4929647 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56528486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gi 3080521 emb CAA18650 - (AL022595) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264890, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gi 3757726 emb CAA18782 - (AL022727) dJ80119.1 (olfactory receptor-like protein [hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	-tm7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gi 4530587 gb AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331828, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56528486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gi1019951 (U37429) - similar to M. musculus MER5 and other AHPC/TSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87188474, 87168559, 265019, 264288, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi15031573[ref NP_005712.1 PACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi13738207[emb CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi1728837[sp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	kinase	264907, 336557402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi14406590[gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi15360093[gb AAD42865.1 AF155099 NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi14757128[emb CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 33696423, 264564, 18108391
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi14884278[emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		264692, 264558, 18108382, 18108385, 264567
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gi13876073[emb CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi1790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 66712502, 56182435, 55811388, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278998, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589680 dbj BAA76859.1 - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264258, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265006, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88098247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657348, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - tRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi 4589642 dbj BAA76843.1 - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906766, 265020, 264693, 18108365, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 284288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gj 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gj 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 29331830, 264908, 264909, 264512, 264910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264638, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gj 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 284259, 60424269, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 284689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gj 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...			struct	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	79846226 (6115, 6116)				UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)				UNCLASSIFIED	264567
3061	87740964 (6121, 6122)				UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi 4454690 gb AAD20963 - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase		264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gi 4240315 db BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain		UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 56181886, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644286, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencode [Homo sapiens]			UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gl 4884268 emb CAB43245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gl 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	struct	264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264689, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)				264112
3069	95412753 (6137, 6138)	Novel Protein sim. GBank gl 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01926) - struct GTPase of unknown function	struct	22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170815, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gij3877788[embjCAB05527] - (283110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gi4502425[refNP_001709.1]pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Thioredoxin	tgf	264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 58182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gi1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptfactor	56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 284555, 56182323, 60432113, 264564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi 134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi 3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264567
3075	880895752 (6149, 6150)	Novel Protein sim. GBank gi 4557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi 3023956 sp Q00808 HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi 3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi 3875410 emb CAB02876 - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	95288274 (6159, 6160)	Novel Protein sim. GBank gi 5257221 gb AAD41265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!!		UNCLASSIFIED	18108398, 264509, 284905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gi 868241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gi 476774 pir A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264368, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264565, 264566, 264567, 264488
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gi 2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gi 3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810764, 263981, 18108385, 264487
3087	87462988 (6173, 6174)				52646365, 58994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gi 3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gi 4689146 gb AAD27782.1 AF07704 - (AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	- dehydrogenase	18108397, 65274572, 56182575, 56181686, 58994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 284486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424179, 52645156, 65274572, 56182575, 56181686, 22278995, 35696286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52844045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21806754, 33109954, 52846317, 55811386, 52844296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264359, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264690, 52844150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22278000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932[emb CAB01859] - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264768, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi 1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - ribosomal prot Ribosomal protein S5	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 29146489, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170615, 264690, 264691, 284692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi 5002587 emb CAB44347.1 - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264564, 264565
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gi 400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35896286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264368, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002, 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	- struct	
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gi 4468288 emb CAB37981 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gi 303603 dbj BAA02145.1 - (D12621) cytochrome P-450L TBV [Homo sapiens]		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gi 1083764 pir B48013 - proline- rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gil5305706 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	sl/uct	35696286, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21906767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gil464564 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	35695917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gil5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22278002, 264563, 264565, 264566, 264486, 264587
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gil1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gil3341441 emb CAA76851 - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906768, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526486, 264482, 264487
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gil5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	56182435, 264288, 264690, 264564

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[emb CAB44347.1] - (Y17454) LSFRI protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	264490, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6219, 6220)	Novel Protein sim. GBank gij1076211[pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264906, 264510, 265006, 265007, 265008, 265009, 60432229, 33657402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906768, 21906767, 21906768, 265020, 60170615, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108365, 18108388, 35698423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3900848 (AC005023) - match to EST AA361117 (NID: g2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gij2459910 (AF005856) - anon2A5 [Drosophila yakuba]		im7	18108397, 22278999, 264259, 29331824, 35698052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gij4966270[gb AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	264909, 56182435, 264910, 21906754
3115	94117996 (6229, 6230)	Novel Protein sim. GBank gij5032225[ref NP_005676.1 pWBSC - Williams-Beuren syndrome chromosome region 11]		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 68712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	79642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gij3880563jembjCAB01444.1] - (Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - Igt EGF-like domain	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35698286, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644286, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265008, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase	
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gij5019819jgbjAAD37863.1jAF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gij4501877jrefjNP_001088.1jpACRj - acrosin		52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)		UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gij2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906784, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87786899 (6247, 6248)		UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gij4980826jgbjAAD35412.1jAE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148827, 29148629, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264369, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35696286, 22278996, 22278999, 29331826, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi 2828280 emb CAA16694.1 - (AL021667) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gi 3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi 3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566, 264636
3130	14993860 (6259, 6260)	Novel Protein sim. GBank gi 3329465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gij4680647[gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646355, 65274572, 56182575, 22278994, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21906754, 52644296, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264389, 52644229, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gij4507613[ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563 264595, 264369, 284685, 264628, 264566
3134	94849816 (6267, 6268)	Novel Protein sim. GBank gij1729827[sp P54633 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			22278998, 264095, 29331826, 33657402, 18108348, 263974
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gjj3093478 (AF012927) - fibrinogen-binding protein [Sireplococcus equi]		struct	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gjj627101[pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486
3137	88257947 (6273, 6274)	Novel Protein sim. GBank gjj3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gij4406759[gijAAD20070] - (AC006636) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109954, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gij228938[prf]1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21906765, 265020, 264636, 264557
3140	91222692 (6279, 6280)	Novel Protein sim. GBank gij932[emb]CAA37773] - (X53744) 68kDA subunit of signal recognition particle [Canis familiaris]	strud		22278995, 56994075, 35696286, 264908, 264909, 60433356, 21908754, 52644298, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35695855, 264630, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE VU1a [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 29331828, 264909, 265009, 285018, 18108351, 264369, 21906768, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gij2498197[sp]Q95245[C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)	cytochrome		52645158, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29146499, 56182435, 265007, 80170831, 60432229, 33657402, 264595, 60433438, 284758, 21906754, 264288, 264766, 264687, 52644229, 21906765, 21906767, 21906768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 284908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264488

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gij488446[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21906766, 21906767, 285020, 265021, 52644150, 27486261, 18108370, 18108374, 35698423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gij3879709[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from t...	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pir]S69890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - struct PH domain		264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gij3874279[emb]CAB07315.1] - (Z92825) predicted using Gensfinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - UNCLASSIFIED haloacid dehalogenase-like hydrolase		56181686, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gb]AAD40851.1[AF08310] - (AF083108) sirutin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij420046 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - eph FYVE zinc finger		29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gij3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - transferase Glutathione S-transferases.		264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - oncogene Zinc finger, C2H2 type		29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52644150, 27486264, 35696423, 22279000

3153	95317299 (6305, 6306)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 52646355, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264369, 264768, 21908765, 21906766, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4680661 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]		ATPase-associated	29331828, 264509, 264905, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264563, 264488
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!		UNCLASSIFIED	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21906769, 35695917, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45821.1 AC00601 - (AC006017) N-acetylglucosaminyltransferase; similar to Q10473 (PID:gi1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35696423, 52644332
3157	88259577 (6313, 6314)				264488, 263974
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306064 gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	56182575, 22278999, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gi3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 264555, 264556, 264557, 264558, 264559

3161	88074111 (6321, 6322)				264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 52644045, 265017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264636, 264566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (UiSMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis , Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH.56.3(UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27(thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (U1MVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen I		

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<210> 4
 <211> 329
 <212> PRT
 <213> Homo sapiens

<400> 4
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 Ala Ala Glu Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His
 35 40 45

Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
 50 55 60
 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
 65 70 75 80
 Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
 85 90 95
 Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
 100 105 110
 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
 115 120 125
 Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
 130 135 140
 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
 145 150 155 160
 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
 165 170 175
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
 180 185 190
 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
 195 200 205
 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
 210 215 220
 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
 225 230 235 240
 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala
 245 250 255
 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
 260 265 270
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
 275 280 285
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
 290 295 300
 Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala
 305 310 315 320
 Glu Gly Arg Lys Ile Leu Glu Glu Phe
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<210> 5

<211> 622

<212> DNA

<213> Homo sapiens

<400> 5

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 180
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 gggtagcagg ggcattgggg taatagcctt ctagcccttt ttgagggaaa cacatgggtg
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aggcctatttt ggggctggga agtggggggc tgggtgtccc tggatggctg tgctggcctc
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 420
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 aactctttct ccactgggat cc
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<210> 6
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 6
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 His Pro Gly Asp Thr Arg Pro Pro Leu Pro Ser Pro Lys Ile Ala Ser
 20 25 30
 Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala
 35 40 45
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
 50 55 60
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
 65 70 75 80
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
 85 90 95
 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
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 Pro Met Ala Arg Arg Glu Thr Val Leu
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<210> 7
 <211> 480
 <212> DNA
 <213> Homo sapiens

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 tgaatgggct ttcagtgtgg ggacagcaaa acatgcacta gggcccagag tggcagttct
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 360

agggtcgtcc tccctgactt gagctctgag ggctttgcct gccagccag agcggcaagg
420
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480

<210> 8
<211> 119
<212> PRT
<213> Homo sapiens

<400> 8
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Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu
20 25 30
Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
35 40 45
Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
50 55 60
Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
65 70 75 80
Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
85 90 95
Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly
100 105 110
Lys Thr Gly Leu Leu Thr Arg
115

<210> 9
<211> 428
<212> DNA
<213> Homo sapiens

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120
tcccagggat gctggatgac ctctttcagt ccatgttcct gtgcgccctg ctgctcttct
180
ggctgtgcgt gtaccacggg attcgtgtcc agggagaaag aaagtgttta actttctatt
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tgccataaatt cttcattggt ggactattgt ggttggtctc tgttacgcta ggaatatggc
300
aaacagttaa cgaattacat gateccaatgt accagtatcg agttgatacc ggaaattttc
360
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420
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428

<210> 10
<211> 138
<212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
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Leu Leu Leu Leu Tyr Asn Asp Pro Phe Phe Pro Leu Ser Phe Leu Val
 20           25           30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
 35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
 50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
 65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
 85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
 100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
 115          120          125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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120
acttgccccg ctcgaccagc acgctgttgg ggtcgtcatg cttcatgccg cccatatcgc
180
catgccccat ggcggcgtgg tccatcttgc ccatgccggg ggccgtgagc atgccgctgg
240
cttgcatctt gagcatttct ttctggtgtt cggcgtgcat cgccgcatca cccagattga
300
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360
catccagagc cttgggcgaa aaggaaatgt cctgcagggt gacttccacg gtgcgcgtgg
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453

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<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
 1           5           10           15
Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

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Cys	Phe	Met	Pro	Pro	Ile	Ser	Pro	Cys	Pro	Met	Ala	Ala	Trp	Ser	Ile
	35		40		45										
Leu	Pro	Met	Pro	Val	Ala	Val	Ser	Met	Pro	Leu	Ala	Cys	Ile	Leu	Ser
	50		55		60										
Ile	Ser	Phe	Trp	Cys	Ser	Ala	Cys	Ile	Ala	Ala	Ser	Pro	Arg	Leu	Asn
65			70		75									80	
Ser	Cys	Ser	Asn	Trp	Pro	Leu	Leu	Thr	Ser	Thr	Lys	Arg	Thr	Val	Ser
			85		90									95	
Pro	Ala	Phe	Thr	Ser	Arg	Ala	Leu	Gly	Glu	Lys	Glu	Met	Ser	Cys	Arg
			100		105									110	
Val	Thr	Ser	Thr	Val	Arg	Val	Ala	Leu	Ser	Ala	Gly	Ala	Gly	Trp	Pro
			115		120									125	
Asn	Ala														
	130														

<210> 13

<211> 2034

<212> DNA

<213> Homo sapiens

<400> 13

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 120
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 180
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 420
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 720
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 780
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 960

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 1080
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 1440
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 1860
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 1920
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 2034

<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

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Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35					40				45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55				60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65					70				75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

85							90					95			
Ala	Ser	Leu	Pro	Ser	Pro	Tyr	Ala	Val	Thr	Gly	Arg	Leu	Leu	Val	Val
100							105					110			
Ser	Ser	Ser	Pro	Tyr	Leu	Gly	Asp	Gly	Arg	Gly	Ala	Ala	Ala	Leu	Arg
115							120					125			
Leu	Leu	Ser	Val	Leu	His	Pro	Asn	Ile	His	Pro	Leu	Leu	Gly	Gln	His
130							135					140			
Trp	Glu	Thr	Thr	Val	Pro	Leu	Leu	Leu	Gly	Tyr	Leu	Asp	Glu	His	Thr
145							150					155			
Glu	Glu	Thr	Leu	Pro	Gln	Glu	Glu	Trp	Glu	Glu	Lys	Leu	Leu	Met	Val
165							170					175			
Arg	Ala	Gly	Val	Arg	Pro	Ile	Leu	Gly	Leu	Lys	Val	Leu	Ser	Gly	Leu
180							185					190			
Gly	Gly	Ala	Gly	Val	Ala	Glu	Ala	Gly	Pro	Pro	Ala	Ser	Thr	Ser	Pro
195							200					205			
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210							215					220			

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<210> 15
<211> 363
<212> DNA
<213> Homo sapiens
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240
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ggt
363
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<210> 16
<211> 121
<212> PRT
<213> Homo sapiens
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<400> 16
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Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
          20          25          30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
          35          40          45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
          50          55          60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

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65		70		75		80									
Ala	Lys	Lys	Tyr	Asp	Leu	Tyr	Thr	Lys	Ile	Thr	Gly	Gly	Gln	Arg	Ile
				85					90					95	
Asp	Leu	Phe	Gly	Ala	Gln	Leu	His	Glu	Leu	Pro	Gln	Ile	Trp	Gly	Glu
			100					105					110		
Leu	Val	Asp	Ala	Gly	Phe	Glu	Thr	Gly							
		115					120								

<210> 17
 <211> 682
 <212> DNA
 <213> Homo sapiens

<400> 17
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 120
 tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
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 agaaacagag cagctggaca agaggacagg tataggggaat aagggagaag ccagtaaggc
 240
 aggaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
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 acccaggtta gaatggtaaa ttgaaagggtg aatataaagg gagaatgggtg aaatgaattt
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 682

<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 18
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20 25 30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
35 40 45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50 55 60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

65		70		75		80									
Phe	Pro	Thr	Pro	Glu	Ile	Pro	His	Ser	Leu	Ala	Pro	Gly	Thr	Val	Ala
			85					90						95	
Ile	Ser	Lys	Pro	Trp	Phe	Pro	Ala	Val	Ser	Gln	Ile	Ala	Arg		
			100					105					110		

<210> 19
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 19
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 120
 cgtctgcagt gcagtcttgg gctataagaa acactgggcc actcaatacc tcccccttt
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 420
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<210> 20
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 20
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 Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
 35 40 45
 Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Leu Trp Ser Met
 50 55 60
 Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
 65 70 75 80
 Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
 85 90 95
 Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
 100 105 110
 Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
 115 120 125
 Lys Ser

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
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 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
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 240
 atacaatgac tgcttgcaact gatgggttca caattgagca attggagctt acacgatctc
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 360
 aattaaagca agttgtccaa ggcatccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
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 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc
 60
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggttc
 180
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta ccgcctgggc
 240
 aacttcctct tcatactgct cggcgtgtgc tgcatttact cgctcttcaa cgtcatctcc
 300
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
 ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttcg
 60
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggtcctct
 240
 gggttgagtg tagggcaaaa gagaaagaag gcaccaagcc tggggtctgg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgccg aggatggaga gagcgatgga gcaactcaac
 60
 cgctgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccaggga taatgaaact
 120
 gctgtttata cattaatgcc aatgggttatg gctgatcaac acaggtctgt ttctgaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65		70		75		80									
His	Ile	Ala	Ala	Asn	Cys	Gly	Ser	Val	Glu	Cys	Leu	Val	Leu	Leu	Leu
			85						90					95	
Lys	Lys	Gly	Ala	Asn	Pro	Asn	Tyr	Gln	Asp	Ile	Ser	Gly	Cys	Thr	
			100					105					110		

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 29
 ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
 60
 gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
 120
 tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
 180
 tactcgctcg tcgtggctgg caatggtcgg ggcctcgtgg gctatggcga aggcaaagat
 240
 actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
 300
 gtatcggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
 360
 tggggcgcta cgcgt
 375

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1 5 10 15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20 25 30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35 40 45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50 55 60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65 70 75 80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85 90 95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100 105 110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115 120 125

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31

accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
 60
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggcccct gagagtgcag
 120
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct
 180
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
 240
 ctgcagagtg cacaaaccta gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
 300
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
 360
 tggcctgcat tgttt
 375 ,

<210> 32

<211> 118

<212> PRT

<213> Homo sapiens

<400> 32

Met	Gln	Ala	Met	Ser	Leu	Lys	Leu	His	Thr	Leu	Trp	Ser	His	Arg	Trp
1				5					10					15	
Gln	Trp	Gln	Pro	Ile	Gly	Ser	Gly	Cys	Cys	Lys	Asp	Val	Ser	Cys	Ser
			20					25						30	
Gly	Gly	Ser	Ala	Ala	Arg	Phe	Val	His	Ser	Ala	Gly	Pro	Thr	Gly	Ala
		35					40					45			
Arg	Asn	Arg	Gln	Glu	Pro	Pro	Phe	Pro	Phe	Glu	Leu	Ala	Gly	Arg	Glu
	50					55					60				
Pro	Cys	Thr	Pro	Arg	Arg	Ser	Cys	Ser	Arg	Pro	Ala	Ala	Ala	Leu	Asp
65					70					75				80	
Pro	Gly	Ile	Ser	Ala	Leu	Ser	Gly	Ala	Gln	Glu	Ala	Ser	Leu	Thr	Arg
			85						90					95	
Arg	Leu	Val	Ser	Ala	Cys	Ser	Arg	Ser	Ser	Pro	Leu	Leu	Ala	Pro	Thr
			100					105					110		
Ser	Ile	Ser	Glu	Gln	Ser										
					115										

<210> 33

<211> 351

<212> DNA

<213> Homo sapiens

<400> 33

ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattt atgggcaacc
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 attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg
 120
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
 180
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggt
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cggtgctagc acagaagtac ataacgggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccacccctca tggaagaaga
 60
 ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggtg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgctctcccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga
 240
 gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggcccgcgt
 300
 ccgacgcttg gtcggggcggg cggggccggg cgcgccaccg cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50           55           60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100          105          110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggaccgcgc
60
gcaaccatga caagggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gateggatct ctccggcgga gtcacgggtgc ttgccgagggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgctcggct gcgcgctggt ctccgacgtgc tggcaccctt gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcggtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca cctcgtctag caggccacac cctcgtcgct cagccccatt
480
gtcatcccgcc gg
492

```

<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

50		55		60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu				
65		70		75
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met				80
	85		90	95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser				
	100		105	110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala				
	115		120	125

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 39
 aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgttaaag agcggtccga tcgccgggaa
 60
 gtgatgngca ccgccaaaat gcaggtgggtc gaagccgcga gttcaggcaa gattgtcttt
 120
 gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
 180
 caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
 240
 ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
 300
 aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
 360
 atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
 412

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1 5 10 15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20 25 30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35 40 45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50 55 60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65 70 75 80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85 90 95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100 105 110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115 120 125
Gln Glu Val Met Val Asn Gly Arg Val

130

135

<210> 41
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 41
gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac
60
tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcactgtggc taaggatttc
120
gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat
180
ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac
240
taccctgatt tccgcgttca cgcgggtgaat ttccctgggg atccgtaccc gatccatctc
300
gacgcgacct ttgtgccgct tcgtccgggg ctcacatca acaacccgaa tcgtccactg
360
ccgcaggagc agaggaagat ctccgaggcc aatgactggc agatcggtga tgctgctcag
420
ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
480
ttggtacttg atccgaagac ggtcatctgc gaggttcgg aagttcatca gatggagcag
540
atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggg
600
ggaggtctcc actgcgccac agctgatgta tatcgccaag gtacctgtga ggactacttc
660
ccgaatcagg tcgacgaccc gaccttggtg tgagaaaacc ccgtgggtcat gtcacgactg
720
acggatctcg gtggctcggg acggaactta cgttgctcgt taccgggccg ccgggtctga
780
tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
840
aacgtcaaac aggaagttcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc
900
atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct
960
gtggatccca cgacgggcag taagtacatc atcggtgatt ttttgccac tggtaggatg
1020
atagtcgggg tcttgggatt tctgcttatt atcgtcatatc ttggaaaatg gtctgagctc
1080

<210> 42
<211> 230
<212> PRT
<213> Homo sapiens

<400> 42
Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
1 5 10 15
Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu

[illegible]

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<210> 43
<211> 358
<212> DNA
<213> Homo sapiens
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<400> 43
gggcccccca catagtggac acagggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggc ctgcagtgcc gggccactgc cacgcacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtccc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgaggggac acagctgcct
300
ccctccgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358
```

```
<210> 44
<211> 105
<212> PRT
<213> Homo sapiens
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<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

1				5					10					15				
Leu	Gly	His	Arg	Gly	Cys	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Ala	Val	Asp			
			20					25					30					
Thr	Thr	Ala	Trp	Ser	Ala	Val	Pro	Gly	His	Cys	His	Ala	His	Arg	Cys			
		35					40					45						
Pro	Leu	Arg	Met	Asp	Leu	Gly	Phe	Arg	Ile	Arg	Val	Ala	Tyr	Gln	Arg			
	50					55					60							
Glu	Ser	Gln	Ile	Leu	Lys	Glu	Val	Gln	Ser	Pro	Glu	Gly	Met	Ile	Ser			
65					70					75					80			
Leu	Arg	Asp	Thr	Ala	Ala	Ser	Leu	Arg	Leu	Glu	Arg	Asp	Thr	Arg	Gln			
			85					90					95					
Leu	Pro	Leu	Leu	Thr	Ser	Ala	Leu	His										
			100					105										

<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

<400> 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcggggtttc
 60
 gcggctcctg gaatcccaga gcagtatggt ggcgacgggtg cggatgcgat tgcgtccgca
 120
 ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat
 180
 gagcttggtta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
 240
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
 300
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
 360
 ggcgttaagg cttgggtcac ggaggctggc gaggccaaagt acctgggtgat atttgcgggt
 420
 actgaccag acgatccgcg ccacagaatc agcgcgttga tgggccatgc agatgaccg
 480
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
 540
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgctc agggcacgg
 600
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagt
 660
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
 720
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
 780
 ttggaggcgg cgcgagcgct gacatactct gcagctgac gtagtgggcg ccagactgac
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 900
 tgcac
 905

<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1 5 10 15
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
 20 25 30
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
 35 40 45
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
 50 55 60
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
 65 70 75 80
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
 85 90 95
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
 100 105 110
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
 115 120 125
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
 130 135 140
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
 145 150 155 160
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
 165 170 175
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
 180 185 190
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
 195 200 205
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
 210 215 220
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
 225 230 235 240
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
 245 250 255
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
 260 265 270
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
 275 280 285
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
 290 295 300

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47
 aagctttag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcatttta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgtcg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagttcat acccgtcggc
 300
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48

<211> 106

<212> PRT

<213> Homo sapiens

<400> 48

Met	His	Leu	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Thr	Glu	Ala	Gly	Cys	His
1				5				10						15	
Ile	Arg	Leu	Ser	Gln	Tyr	Ala	Arg	Lys	Val	Arg	Gln	Thr	Gln	Leu	Arg
		20						25					30		
Val	Glu	Tyr	Leu	Arg	Leu	Arg	Leu	Ala	Ser	Leu	Pro	Gly	Gly	Asp	Ala
		35					40					45			
Gly	Ala	Ala	Val	Gly	Ile	Asp	Arg	Arg	Leu	Arg	Leu	Asp	Phe	Glu	Lys
	50					55					60				
Gly	Leu	Thr	Lys	Ser	Gln	Gly	Arg	Arg	Glu	Glu	Phe	Ile	Pro	Val	Gly
65				70					75					80	
Glu	Asp	Ala	Ser	Thr	Tyr	Asn	Arg	Leu	Met	Lys	Ala	Leu	Arg	Gln	Arg
			85					90						95	
His	Asp	Val	Ile	Lys	Ser	Gly	Lys	Leu	Ala						
		100						105							

<210> 49

<211> 309

<212> DNA

<213> Homo sapiens

<400> 49

tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgctcg
 180
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacaggga aactcttcaa
 240
 aaagttatct ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctctttttg
 309

<210> 50

<211> 101

<212> PRT

<213> Homo sapiens

<400> 50

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Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1             5             10             15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
          20             25             30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
      35             40             45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50             55             60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65             70             75             80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
          85             90             95
Val Leu Pro Pro Phe
          100

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<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

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agatctttga agaattgccca cactgtcttc ctccctgctt ataatttctt tattccctag
60
gatgtgatcc ttgttcttgg ggcctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccctt
300
caaaatcttc tggtgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctccca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1             5             10             15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20             25             30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

35			40			45									
Ser	Cys	Thr	Ser	Cys	Ala	Pro	Gln	Asn	Leu	Leu	Leu	Leu	Arg	Glu	Lys
50			55			60									
Arg	Pro	Ala	Gly	Ile	Glu	Gln	Leu	Ala	Leu	Ser	Ala	Ser	Ala	Ser	
65			70			75			80						
Gln	Gly	Asp	Val	Gly	Val	Leu	Asn	Pro	His	Arg	Gly	Cys	Gly	Pro	Leu
85			90			95									
Arg	Leu	Gly	Trp	Met	Gly	His	Gln	Val	Gly	Pro	Leu	Phe	His	Leu	Cys
100			105			110									
Asp	Leu	Pro	Ser	Gly	Leu	Leu	Val	Gly	Ser	Cys	Phe	Leu			
115			120			125									

```
<210> 53
<211> 474
<212> DNA
<213> Homo sapiens
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```
<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gagggccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcacgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgegggt acgtaaccgt
300
gaccaagtcg acgggcgctc ccgcggtac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474
```

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<210> 54
<211> 101
<212> PRT
<213> Homo sapiens
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```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
  1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
          20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
          35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
  50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
          85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagccgg catatcggtt acgactacgg tacaccggtg gcgccacagt
 60
 tcggcgcagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
 120
 tgggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
 180
 agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcgtttca
 240
 gccgcatcgg catgggcctg gtggatgaca agggccggtg cattaccacg ggcgtatcgc
 300
 gcgcgttgaa tgcggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggg gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atcctgggaa ctagccgtga caagggtcaat cacatgatta tcgacggcga ggaacgggat
 300
 atgggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcgggtg gcaccgcca gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatgggtt ggggtgaagtc gtggcttctg ctccaccag
 60
 tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaact
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacggtga
360
tgctttcaga agcccgggag agcgtcttgg gggcagtgct gaagggttggtg ctgtaca
417

<210> 60
<211> 101
<212> PRT
<213> Homo sapiens

<400> 60
Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
1 5 10 15
Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
20 25 30
Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
35 40 45
Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
50 55 60
Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
65 70 75 80
Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
85 90 95
Lys Val Val Leu Tyr
100

<210> 61
<211> 304
<212> DNA
<213> Homo sapiens

<400> 61
agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccctatcc
60
gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
120
tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
180
ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
240
tcccctagac cgggcccattg gccaggcctg accacagagc tcccattgcc tttcctgcac
300
gcgt
304

<210> 62
<211> 92
<212> PRT
<213> Homo sapiens

<400> 62
Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
 cgcgtcaagg gggctctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
 60
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtgggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccga ccacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgcctcaatc ggtctgtgac gccttggccg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgcagc cgcctcaacc ctgcccacg gcgtcgtctg
 480
 gtgctgggtg ctccccgctc ccccgaactg ttcgacgata ctgcccgctg gaacatcgtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

```

<210> 65

<211> 339

<212> DNA

<213> Homo sapiens

<400> 65

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gtcgaccgcg ccttgggatc gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcgc gggcaactag tgggcacccat ggccctccgag
120
cgcccttggcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatect tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggccctgcccc
300
cgcgtcggcg gtttgtctgg ctcccttcac cggggtcc
339

```

<210> 66

<211> 113

<212> PRT

<213> Homo sapiens

<400> 66

```

Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
20     25     30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
35     40     45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
50     55     60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65     70     75     80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
85     90     95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
100    105    110

```

Ser

<210> 67

<211> 446

<212> DNA

<213> Homo sapiens

<400> 67

tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc
 60
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
 120
 caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
 180
 gggagtcggg cccgccctag ccttcctcga ttcagcgtgg ggacgccaga tccacgtgga
 240
 gacaacaggg tgtcccagtg ccgtggtctg gaatccacgc tcctcgtcga cacatgccga
 300
 taaccgcgaca gccacggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
 360
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga
 420
 aacgttgtga tcgctgcatt gatatt
 446

<210> 68

<211> 133

<212> PRT

<213> Homo sapiens

<400> 68

Met	Trp	His	Thr	Tyr	Leu	Arg	Val	Ala	Asp	Ala	Ala	Gln	Ala	Arg	Val
1				5					10					15	
Arg	Gly	Val	Arg	Gly	Ala	Ser	Trp	His	Asn	Phe	Ala	Thr	Gly	Asp	Lys
			20					25					30		
Gly	Ser	Phe	Asp	Ala	Asn	Glu	Leu	Ala	Val	Thr	Pro	Asp	Thr	Asp	Thr
		35					40					45			
Val	Ile	Gln	Gly	Val	Gly	Pro	Ala	Leu	Ala	Leu	Leu	Asp	Ser	Ala	Trp
	50					55					60				
Gly	Arg	Gln	Ile	His	Val	Glu	Thr	Thr	Gly	Cys	Pro	Ser	Ala	Val	Val
65					70					75				80	
Trp	Asn	Pro	Arg	Ser	Ser	Ser	Thr	His	Ala	Asp	Asn	Pro	Thr	Ala	Gln
				85					90					95	
Ala	Trp	Arg	Asp	Phe	Val	Cys	Val	Glu	Thr	Gly	Ala	Cys	Lys	Asp	Asn
			100					105					110		
Ala	Val	Ile	Val	Ala	Pro	His	Ser	Asp	Leu	Thr	Met	Ser	Thr	Arg	Ile
		115					120					125			
Ser	Val	Glu	Thr	Leu											
															130

<210> 69

<211> 552

<212> DNA

<213> Homo sapiens

<400> 69

nnaagggtaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
60
ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccagag atgccaaaaa
120
agtcttccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccagaagg
180
agcncctatgg ccccttcctt cagtgggaata ccaaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgccccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgac
540
ctttcctgta ca
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
			20					25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
		50				55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65					70				75					80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
				85					90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys
		115					120					125			
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
		130				135					140				
Ser	Gly	Ser	Val	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser
145					150					155				160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
				165					170					175	
Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
				180											

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 71
 cgcggttgaaa tggcggttcga acttaaactg ttacatattg actccgtgcc attaaacatt
 60
 ttgaatcctg ttaaagggac tccatttgaa agcaacgaag ctttacgtcc tttaaataac
 120
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtgg cctaaacggt
 240
 atcatggttg gtggctactt aactactggc ggtcggtcac ctcaagacga tctccaaatg
 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
 1 5 10 15
 Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn
 20 25 30
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
 85 90 95
 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
 nntaccggca agatcctggc cgaaggtgac gtcgaggttt ctgaggctat cgactttgct
 60
 gcttggtatg tcgaccgagc cgaggagctc gagggcgctc acggtgcca gtttggtgccg
 120
 ccacgagtga ccgtcgtcac ccgcgcgtgg aacttcgccc tgtctattac cgccggatcc
 180

acccttgccg ctctggccgc cggatcgta gtactactca agcccgtcc acaggcccgc
 240
 cactgtgctg ccgtcatctc tgaatgcctg tgggaggctg ggatcccgcg ggacgttctg
 300
 cagctcgctg atgttgagga aaatgaggct ggtaaacacc tggtagacca ccccgaggtc
 360
 gatcgggtca tcctcacggg aggt
 384

<210> 74
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 74
 Xaa Thr Gly Lys Ile Leu Ala Glu Gly Asp Val Glu Val Ser Glu Ala
 1 5 10 15
 Ile Asp Phe Ala Ala Trp Tyr Val Asp Arg Ala Glu Glu Leu Glu Gly
 20 25 30
 Val Asp Gly Ala Gln Phe Val Pro Pro Arg Val Thr Val Val Thr Pro
 35 40 45
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
 50 55 60
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
 65 70 75 80
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
 85 90 95
 Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys
 100 105 110
 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
 115 120 125

<210> 75
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 75
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<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
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 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
 50 55 60
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
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 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
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 <213> Homo sapiens

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<210> 78

<211> 799

<212> PRT

<213> Homo sapiens

<400> 78

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Thr	Ala	Ser	Ile	Ile	Gly	Asp	Val	Met	Gly	Pro	Thr	Leu	Asn	His	Leu	35	40	45	
Asn	Asn	Leu	Leu	Arg	Leu	Pro	Phe	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	50	55	60	
His	Phe	Ala	Pro	Asn	Val	Phe	Val	Leu	Lys	Tyr	Leu	Gln	Lys	Thr	Gln	65	70	75	80
Gln	Leu	Ser	Pro	Glu	Val	Glu	Arg	Glu	Thr	Thr	Asp	Tyr	Leu	Val	Gln	85	90	95	
Gly	Tyr	Gln	Arg	Gln	Leu	Thr	Tyr	Lys	Arg	Gln	Asp	Gly	Ser	Tyr	Ser	100	105	110	
Ala	Phe	Gly	Glu	Arg	Asp	Ala	Ser	Gly	Ser	Met	Trp	Leu	Thr	Ala	Phe	115	120	125	
Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Ser	Phe	Ile	Phe	Val	Asp	Pro	130	135	140	
Arg	Glu	Leu	Ala	Ala	Ala	Lys	Ser	Trp	Ile	Ile	Gln	Gln	Gln	Gln	Ala	145	150	155	160
Asp	Gly	Ser	Phe	Leu	Ala	Val	Gly	Arg	Val	Leu	Asn	Lys	Asp	Ile	Gln	165	170	175	
Gly	Gly	Ile	His	Gly	Ile	Val	Pro	Leu	Thr	Ala	Tyr	Val	Val	Val	Ala	180	185	190	
Leu	Leu	Glu	Thr	Gly	Thr	Ala	Ser	Glu	Glu	Glu	Arg	Gly	Ser	Thr	Asp	195	200	205	
Lys	Ala	Arg	His	Phe	Leu	Glu	Ser	Ala	Ala	Pro	Leu	Ala	Met	Asp	Pro	210	215	220	
Tyr	Ser	Cys	Ala	Leu	Thr	Thr	Tyr	Ala	Leu	Thr	Leu	Leu	Arg	Ser	Pro	225	230	235	240
Ala	Ala	Pro	Glu	Ala	Leu	Arg	Lys	Leu	Arg	Ser	Leu	Ala	Ile	Met	Arg	245	250	255	
Asp	Gly	Val	Thr	His	Trp	Ser	Leu	Ser	Asn	Ser	Trp	Asp	Val	Asp	Lys	260	265	270	
Gly	Thr	Phe	Leu	Ser	Phe	Ser	Asp	Arg	Val	Ser	Gln	Ser	Val	Val	Ser	275	280	285	
Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Tyr	Thr	Leu	Leu	290	295	300	
Gly	Asp	Val	Ala	Ala	Ala	Leu	Pro	Val	Val	Lys	Trp	Leu	Ser	Gln	Gln				

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Arg	Asn	Ala	Leu	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Cys	Val
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Leu	Gln	Ala	Leu	Ala	Glu	Tyr	Ala	Ile	Leu	Ser	Tyr	Ala	Gly	Gly
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Asn	Leu	Thr	Val	Ser	Leu	Ala	Ser	Thr	Asn	Leu	Asp	Tyr	Gln	Glu
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Phe	Glu	Leu	His	Arg	Thr	Asn	Gln	Lys	Val	Leu	Gln	Thr	Ala	Ile
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Pro	Ser	Leu	Pro	Thr	Gly	Leu	Phe	Val	Ser	Ala	Lys	Gly	Asp	Gly
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Cys	Leu	Met	Gln	Ile	Asp	Val	Thr	Tyr	Asn	Val	Pro	Asp	Pro	Val
			405					410				415		
Lys	Pro	Ala	Phe	Gln	Leu	Leu	Val	Ser	Leu	Gln	Glu	Pro	Glu	Ala
		420					425				430			
Gly	Arg	Pro	Pro	Pro	Met	Pro	Ala	Ser	Ala	Ala	Glu	Gly	Ser	Arg
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Asp	Trp	Pro	Pro	Ala	Asp	Asp	Asp	Asp	Pro	Ala	Ala	Asp	Gln	His
450					455				460					
Gln	Glu	Tyr	Lys	Val	Met	Leu	Glu	Val	Cys	Thr	Arg	Trp	Leu	His
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Gly	Ser	Ser	Asn	Met	Ala	Val	Leu	Glu	Val	Pro	Leu	Leu	Ser	Gly
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Arg	Ala	Asp	Ile	Glu	Ser	Leu	Glu	Gln	Leu	Leu	Leu	Asp	Lys	His
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Gly	Met	Lys	Arg	Tyr	Glu	Val	Ala	Gly	Arg	Arg	Val	Leu	Phe	Tyr
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Thr	His	Ser	Pro	Leu	Ala	Arg	Glu	Leu	Cys	Ala	Gly	Pro	Ala	Cys
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Glu	Val	Glu	Arg	Ala	Pro	Ala	Arg	Gly	Pro	Gly	Trp	Phe	Pro	Gly
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Ser	Gly	Pro	Ala	Val	Ala	Pro	Glu	Glu	Gly	Ala	Ala	Ile	Ala	Arg
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Gly	Cys	Asp	His	Asp	Cys	Gly	Ala	Gln	Gly	Asn	Pro	Val	Cys	Gly
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Asp	Gly	Val	Val	Tyr	Ala	Ser	Ala	Cys	Arg	Leu	Arg	Glu	Ala	Ala
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Glu	Gln	Arg	Leu	Pro	Ala	Ser	Ser	Ser	Ser	Thr	Tyr	Gly	Asp	Asp
	675				680				685					
Ala	Ser	Val	Ala	Pro	Gly	Pro	Leu	Gln	Gln	Asp	Val	Lys	Leu	Asn
690				695				700						
Ala	Gly	Leu	Glu	Val	Glu	Asp	Ser	Asp	Pro	Glu	Pro	Glu	Gly	Glu
705				710				715					720	
Glu	Asp	Arg	Val	Thr	Ala	Gly	Pro	Arg	Pro	Pro	Val	Ser	Ser	Gly
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Leu	Glu	Ser	Ser	Thr	Gln	Ser	Ala	Ser	Pro	Phe	His	Arg	Trp	Gly

			740					745					750			
Thr	Pro	Ala	Pro	Gln	Arg	His	Ser	Gly	Arg	Val	Val	Gly	Ala	His	Arg	
		755					760					765				
Pro	Gly	Leu	Leu	Ser	Pro	Val	Phe	Val	Tyr	Ser	Pro	Ala	Phe	Gln	Ser	
	770					775					780					
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<210> 79
<211> 346
<212> DNA
<213> Homo sapiens
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<210> 80
<211> 101
<212> PRT
<213> Homo sapiens
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Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
          35          40          45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
          50          55          60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
65          70          75          80
Ser Glu Glu Ala Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
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Pro Asp Gly Asn Ala
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<210> 81
<211> 429
<212> DNA
<213> Homo sapiens
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<400> 81

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<210> 82
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 82
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<210> 83
 <211> 411
 <212> DNA
 <213> Homo sapiens

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 411

<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
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 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
 100 105 110
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
 115 120 125

<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 120
 acccagcggtt tcttggtgga gaacggagta ccggcggaaa agatcaacaa ggtgctggaa
 180
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc
 240
 accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgcac
 300
 aaagtgccat attacaccac tctttcaggt gca
 333

<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr
 1 5 10 15
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
 20 25 30
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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      35      40      45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
      50      55      60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65      70      75      80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85      90      95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100      105      110

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<210> 87
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 87
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 ctccctgagcg atgttcattc ggtaggggta caggggtgacg ggcgtactta tggttctccc
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 attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
 180
 tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
 240
 gtgggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
 300
 caccgtgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gttag
 355

<210> 88
 <211> 96
 <212> PRT
 <213> Homo sapiens

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<400> 88
Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
 1      5      10      15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20      25      30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35      40      45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50      55      60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65      70      75      80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85      90      95

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<210> 89
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 89

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 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca
 120
 ggtgattgga taaggccaga gggttgggcg gggttctgcc cctgctgaag cctgggtggg
 180
 ccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
 240
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc
 300
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c
 351

<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90
 Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser
 1 5 10 15
 Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser
 20 25 30
 Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg
 35 40 45
 Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile
 50 55 60

<210> 91
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 91
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 acgtcgaagc ccagcagggc ctctcgcagg tccctggggc agccagcaca cacaagtc
 120
 cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct
 180
 gcctcttgca ggtactgctc gggctctggtg ggagggcagc cgtgtccagc acaccctgtg
 240
 tgtgcagtcc tctccctgcc ccactgccga acgagccctc cacgggtgaag ccattgggga
 300
 acgtgacctt gcccttcccc atgaggt
 327

<210> 92
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

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1           5           10           15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20           25           30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35           40           45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50           55           60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
65           70           75           80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85           90           95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100           105

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<210> 93

<211> 394

<212> DNA

<213> Homo sapiens

<400> 93

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nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
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120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataatcccg ggcgccacct gatcgtgacc gagggtagca aaacggaacc
240
gctctatttc gaggtatca ggttgctgtt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcggaagaa agtgccacag gattcactca cgta
394

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<210> 94

<211> 109

<212> PRT

<213> Homo sapiens

<400> 94

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Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
1           5           10           15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20           25           30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35           40           45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
50           55           60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65           70           75           80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85           90           95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

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100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tgcttgatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc
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 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
 240
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcacc catgccatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttcct
 480
 aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97

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 tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg cgccgtagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagcttt ggcgctccagg cgcgctcggg
 180
 cggtcggccc tcttgccgga attgattcag cgcaatcccg gccatcacat gccagcgctt
 240
 gtccaggggc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98

<211> 122

<212> PRT

<213> Homo sapiens

<400> 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40					45			
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55				60					
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65					70				75					80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85					90						95	
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
		100					105						110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
		115					120								

<210> 99

<211> 545

<212> DNA

<213> Homo sapiens

<400> 99

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 120
 tcgatcccat cactcgggat ttgctggaat ccctggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcggtcgca tcgattggct ctccccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc
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 ccattccacg atcagggttaa ggtggccggc ggtggtggtt ctgctcctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga
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 540
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 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Gly Thr Phe Ser His His Arg Val Pro Pro Glu Asp Asp Ser Lys
 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
 100

<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 120
 aagctgccgg gggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

gtcgacattg tccacgcaa agatgtccat aaggagatgg ccgacaagct tttgcctggc
 480
 gagatcacct ggtccgaagg cattegcgcc gggatgttcg cacccatcgg cgacgggtgat
 540
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 600
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<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
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 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
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 gccattgggg ggagaccct gccgtgggga aagaccctg ccatggggca gaccctgcc
 120
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc
 180
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccgt
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 300

agtgggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gaggggttgg cgcacggtec actccgtggc gcccggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcacg gccccagcgg tcggcatccc agccgtggtc gccgtcgagc gccccaggg
240
cctcaatgtc gtcacggcg gccagttcca cccggcgga catctcgttg cggaccatga
300
cccgggaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

	35		40		45
Arg	Arg	Pro	Val	Pro	Pro
				Gly	Gly
				Thr	Ser
				Arg	Cys
					Gly
					Pro
50			55		60

<210> 107

<211> 549

<212> DNA

<213> Homo sapiens

<400> 107

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60gccgcttaat aaccgaccaa catgaaactc aagggtgcc ccttcctagc ggggaccctg
120cacagaccgc aaaataaggc gttttgctct gccctcctca gttcacgtgg gcaccttgga
180acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcactgtttt
240cgctccttc gccctgttct cgtgactgac aggagcaggc gtcacaagca ggcagcccga
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360ggcctgttgt cctcctccac atgcgcccat cttcactctt tcatgtgact ggctgtttt
420tgaaggcaag gccctgtca cccttggtta ggccaggtat gttctgcacc gaaaatggcc
480ctgccctctg cattggatgg ctagctctta gggttggtta ttttagcaaa taagcggtac
540

agggtaggc

549

<210> 108

<211> 108

<212> PRT

<213> Homo sapiens

<400> 108

Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
1 5 10 15Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
20 25 30Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
35 40 45Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
50 55 60Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
65 70 75 80Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
85 90 95Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
100 105

<210> 109

<211> 748

<212> DNA

<213> Homo sapiens

<400> 109

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aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataatgagt
120
gatattgggg taagttacca atttacttta cagcccttaa gtataataatc tgctttcctc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
300
gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
360
atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcattggcag
420
aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
480
ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
540
cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
600
aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
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gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
720
cacagagagt caatggaggg cttccgga
748

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<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

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Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1      5      10      15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20      25      30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35      40      45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50      55      60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65      70      75      80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85      90      95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100     105     110
Val Leu Ala Phe Gln Thr Met Glu Glu Lys Glu Lys Glu Gln Arg
115     120     125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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130 135 140
 Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg
 145 150 155

<210> 111
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 111
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 120
 tcggcttatn nacgccacca gcatncgact ttggctgaga tcatcgcacc gttcggacat
 180
 ctggtcatga tcgacggaac cgactcatte gatctcatgg ccttcaagtc aaagtcgtta
 240
 acggtgacca gcgagtcgat gttcagccgt ccacagttcg cgacgcccga cgtcgccgaa
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 caaggccggg cactggccag catcgccgac ctctctgaga aggggcagat ccgtccgacg
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 420
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 429

<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 112
 Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly
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 Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly
 20 25 30
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
 35 40 45
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
 115 120 125
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Val Glu Ser Gly
 130 135 140

<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

<400> 113

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 120
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggcttc
 180
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<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

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<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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<210> 116

<211> 1062

<212> PRT

<213> Homo sapiens

<400> 116

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Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg			
35	40	45	
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile			
50	55	60	
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr			
65	70	75	80
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg			
85	90	95	
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg			
100	105	110	
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val			
115	120	125	
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe			
130	135	140	
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu			
145	150	155	160
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu			
165	170	175	
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser			
180	185	190	
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu			
195	200	205	
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg			
210	215	220	
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser			
225	230	235	240
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro			
245	250	255	
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro			
260	265	270	
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg			
275	280	285	
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg			
290	295	300	
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser			
305	310	315	320
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu			
325	330	335	
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln			
340	345	350	
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys			
355	360	365	
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala			
370	375	380	
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys			
385	390	395	400
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu			
405	410	415	
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro			
420	425	430	
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln			

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Gln	Cys	Gln	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln		
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Tyr	Phe	Glu	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala		
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Arg	His	Ser	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys		
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Gln	Thr	Gln	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu		
	500					505					510						
Ala	Thr	Arg	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr		
	515					520					525						
Arg	Ala	Glu	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln		
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Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala		
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Arg	Pro	Pro	Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro		
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Asn	Thr	Gly	Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu		
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Ala	Val	Leu	Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Gly		
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625						630					635					640	
Gln	Arg	Ile	Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln		
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Lys	His	Gly	Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu		
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Ile	Glu	Glu	Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile		
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Val	Gly	Gln	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp		
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Glu	Ser	Leu	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro		
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Ala	Leu	Thr	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala		
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Pro	Ile	Gly	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp		
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785						790					795					800	
Leu	Pro	Leu	Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu		
	805					810					815						
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	820					825					830						
Leu	Cys	Thr	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala		
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Gln	Gly	Thr	Ala	Leu	Gly	Ala	Val	Leu	Gly	Leu	Ser	Trp	Arg	Arg	Gly		
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Leu	Met	Gly	Val	Pro	Leu	Gly	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Ala	Trp		

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Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
          900          905          910
Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
          915          920          925
Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
          930          935          940
Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
945          950          955          960
Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
          965          970          975
Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
          980          985          990
Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
          995          1000          1005
Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
          1010          1015          1020
Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
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Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg
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<210> 117
<211> 471
<212> DNA
<213> Homo sapiens

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<210> 118
<211> 157
<212> PRT
<213> Homo sapiens

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<400> 118

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      20           25           30
Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
      35           40           45
Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
      50           55           60
Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
65           70           75           80
Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
      85           90           95
Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
      100          105          110
Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
      115          120          125
Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
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Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
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<210> 119

<211> 302

<212> DNA

<213> Homo sapiens

<400> 119

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<210> 120

<211> 98

<212> PRT

<213> Homo sapiens

<400> 120

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      20           25           30
Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
      35           40           45
Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

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<210> 121
 <211> 318
 <212> DNA
 <213> Homo sapiens

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 318

<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 122
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 Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
 35 40 45
 Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
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 Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
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<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

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<210> 124
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala
 1 5 10 15
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu
 20 25 30
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
 35 40 45
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
 50 55 60
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
 65 70 75 80
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
 85 90 95

<210> 125
 <211> 280
 <212> DNA
 <213> Homo sapiens

<400> 125
 ccattggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 tccccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcctggccca ttctggatag gcctgatcta
 280

<210> 126
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1           5           10           15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20           25           30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35           40           45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50           55           60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
      65           70           75           80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85           90

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<210> 127

<211> 444

<212> DNA

<213> Homo sapiens

<400> 127

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cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcacga ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcca tgcggcctg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggtcg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgccctgatc gccaggatgg ccactgtgcg caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128

<211> 148

<212> PRT

<213> Homo sapiens

<400> 128

```

Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
      1           5           10           15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20           25           30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35           40           45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50           55           60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
      65           70           75           80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85           90           95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

100 105 110
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
 115 120 125
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
 130 135 140
 Lys His Trp Cys
 145

<210> 129
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 129
 gaggagggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac
 60
 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgtc
 120
 gagtgcccgc tcgaggaagt tccgctgac caaaagcaga tcatcgagaa ggctcgttta
 180
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctccccgt
 240
 ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
 291

<210> 130
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 130
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
 1 5 10 15
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
 20 25 30
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro
 35 40 45
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
 50 55 60
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
 65 70 75 80
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
 85 90 95
 Ala

<210> 131
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 131
 tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag
 60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggg acgggttact gccgacgtcg acgcggtggt ggacatggtc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc
 416

<210> 132

<211> 126

<212> PRT

<213> Homo sapiens

<400> 132

Ser	Gly	Ala	Ser	Val	Ala	Leu	Met	Gly	Val	Ser	Ala	Trp	Leu	Leu	Ser
1				5				10					15		
Arg	Ala	Ala	Glu	Ile	Pro	Pro	Val	Leu	Tyr	Leu	Glu	Ala	Ala	Ala	Val
			20					25					30		
Gly	Val	Arg	Phe	Phe	Gly	Ile	Ser	Arg	Gly	Val	Phe	Arg	Tyr	Ala	Glu
			35				40					45			
Arg	Leu	Val	Gly	His	Asp	Leu	Ala	Leu	Arg	Met	Gln	Gly	Ala	Leu	Arg
			50				55				60				
Met	Arg	Val	Tyr	Asp	Arg	Leu	Ser	Arg	Thr	Xaa	Pro	Ala	Gly	Xaa	Arg
							70				75				80
Arg	Arg	Gly	Asp	Leu	Leu	Val	Arg	Val	Thr	Ala	Asp	Val	Asp	Ala	Val
							85				90			95	
Leu	Asp	Met	Val	Val	Arg	Val	Ile	Val	Pro	Ala	Cys	Ala	Ser	Ser	Leu
							100				105			110	
Val	Ile	Ile	Gly	Thr	Thr	Val	Leu	Leu	Cys	Pro	Arg	Glu	Gly		
							115				120			125	

<210> 133

<211> 327

<212> DNA

<213> Homo sapiens

<400> 133

gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct
 60
 gcggtgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccaccgcg
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttggtga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaaagct tggtactacc gatatgggtg ctcacatgca gcctgggtct
 240
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact
 300
 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
 60
 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagttggc ttttcttggg ggattggaaa catcctcttg gaggcaaaga cttttcctgg
 180
 atcttacaga cttcccgga ttttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcacgc tcgagagaga attacttcac tggctccact tggagtgcc
 480
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg
 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

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Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
 20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
 35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
 65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
           85           90           95
Ile Ser Ser Gly
           100

```

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

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accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcata gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgata ggcagcgcct ggctggcgcc ctggtcgagc
240
cagcgcgteg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggatc acggcaagtg
360
ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

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Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
 20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
 35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

65		70		75		80									
Gln	Ser	Gly	Phe	Val	Glu	Asp	Leu	Phe	Arg	Ser	Gln	Val	Ala	Asp	Lys
			85						90					95	
Thr	Asn	Trp	Arg	Ala	Leu	Leu	Lys	Gly	Asp	Ala	Gln	Ser	Val	Asp	Leu
			100					105					110		
Lys	Gln	Val	Arg	Asp	Gln	Leu	Phe	Ala	Ser	Cys	Ala	Glu	Gly	Leu	Leu
		115				120						125			
Ser	Leu	Gln	Glu	Arg	Phe	Gly	Leu	Gln	Ala	Ile	Gln	Pro			
	130					135					140				

<210> 139
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 139
 acgcgtcgtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
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 ttgtgaacag cagaatcaag ccgctggtaa atcttcctgg gagcttcata ggcggggatg
 120
 ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
 180
 tttgcagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
 240
 acggccactt caccgatctc ttcataagccc tggcggtttgt agaaatccag gtagcgcgaa
 300
 tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
 341

<210> 140
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1 5 10 15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
20 25 30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
35 40 45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50 55 60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65 70 75 80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
85 90 95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
100 105 110
Ala

<210> 141
 <211> 324

<212> DNA

<213> Homo sapiens

<400> 141

gaattcctct tggatagctt cgggtaaagt ggtacagcaa atatcaggag cgcaaccgca
 60
 acctttactt actggtacat gaacaccatt tacattacag ctatcgtaact cacccccacgt
 120
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
 180
 gtcaactgtg aacaccgcta agtaatagcc tgcggggggt tgcatagaact cctttgacca
 240
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
 300
 gcagttatca ccgcccatac gcgt
 324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
	35						40				45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50					55					60				
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70						75				80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85					90					95		
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100					105							

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
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 gcaccccagg agaagaactt cctgtacaaa tgcataaggca ccaccctggg tgctgcttca
 120
 agtaaggagg tggtagaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
 180
 gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag
 240
 gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
 300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaaggtgaa gagtgtctctg
 360
 atcctgtgct atgggcacgt ggcggcccgg gccccccggg agctgggtgct ggccaaggta
 420
 gagtcagaca tcctccggaa catcntgccg gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaagca gagctgggtg cacagatgat ggagttcatc
 600
 agggcagagc ccccggactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccggggcgga tgtgatccat
 720
 ggctgctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
 840
 cagcggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtccccaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggatcc tgtgcaatgg cctgggtgcc cttccacaac ctgggccttc tcatcggcct
 1080
 cttctcccca cgggtgtgcg acctgtggcc tgccaccgcg caggaggccg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggtta tgagggcttc tcccgggact accgcgatga
 1200
 cgtggcgag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
 1260
 cttccacacc tgccacagtg taggccagat tattgccaag cgcctccccc cagcccttca
 1320
 cgcgt
 1325

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Xaa	Ala	Trp	Ile	Cys	Gln	Leu	Ser	Leu	Glu	Leu	Cys	Arg	Gln	Leu	Pro
1				5					10					15	
Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
			20					25					30		
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Lys	Glu	Val	Val	Arg	Lys	His	
		35					40					45			
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
		50				55					60				
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
65				70					75					80	
Asp	Thr	Leu	Ala	Gln	Leu	Glu	Asp	Phe	Val	Arg	Ser	Glu	Val	Phe	Arg

[illegible]

<210> 145

<211> 802

<212> DNA

<213> Homo sapiens

<400> 145

cggccgtcta ggtccggctc agtgcgctgt tgctcgccgt agaacacgag gctgcgcaag
60

cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggctc
120

180
acatcaccct ggtgaaggcc tgcaccacta gcgctcggcac catttccccg cgtcggacaa
180

gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240

cagaggacga caccgatctg gcggacgccg cccgttcacg gcgcagatac ctcacccctc
 300
 tcatttggtg cgttatcgtc gctgtcctcg gactagggat ttccgggtat cttgcgtggg
 360
 ggccattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaacccggt atgtactggg
 420
 gtccgggtgg ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctgggtggc acatgcttgcca tcgtcatccc ggctgttttc atcgtcgcgc
 540
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
 600
 tattgatctc cgttttatcg gctcctagca gccgtgggtc acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttgttggt ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaatcccatt
 780
 ctcgatagac ggccccacac ac
 802

<210> 146
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Lys Val Tyr Ile Thr Leu Val Lys Ala Cys Thr Thr Ser Val Gly
 1 5 10 15
 Thr Ile Ser Pro Arg Arg Thr Arg His His Ala Pro Tyr Leu Asp Arg
 20 25 30
 Met Ser Asp Met Ser Met Pro Arg Arg Ala Ala Pro Glu Asp Asp Thr
 35 40 45
 Asp Leu Ala Asp Ala Ala Arg Ser Trp Arg Arg Tyr Leu Ile Leu Val
 50 55 60
 Ile Cys Gly Val Ile Val Ala Val Leu Gly Leu Gly Ile Phe Gly Tyr
 65 70 75 80
 Leu Ala Trp Trp Ser Leu Cys Asp Gln Ala Ala Gly Val Cys Gln Arg
 85 90 95
 Gly Glu Pro Val Met Tyr Trp Cys Ser Val Val Ser Leu Ala Ile Leu
 100 105 110
 Gly Leu Ile Ile Gly Val Leu Thr Gln Ile Trp Leu Glu Lys Arg Trp
 115 120 125
 Trp His Met Leu Ala Ile Val Ile Pro Ala Val Phe Ile Val Ala Gly
 130 135 140
 Ile Phe Phe Trp Leu Ala Val
 145 150

<210> 147
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 147

acgcgtgaaa acggtatgac tcttctggcc ttagtagatc tgtctaaaaa acccgatgag
 60
 ttacacacagt gggcattagt agcccgcgat gttcatgaca ttcttgggtct acgaaaagtt
 120
 attggtcaga aagtaccttg tggtgcagtg acggggtcgg aaaagggtgct tcataaaaag
 180
 gattactggg atctagcaac acctatgcca attgcgtggg gtacaacgga ccgaacagtt
 240
 attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt
 300
 ccacgcctag aagagggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148

<211> 117

<212> PRT

<213> Homo sapiens

<400> 148

Met	Thr	Leu	Leu	Ala	Leu	Val	Asp	Leu	Ser	Lys	Lys	Pro	Asp	Glu	Phe
1				5					10					15	
Thr	Gln	Trp	Ala	Leu	Val	Ala	Arg	Asp	Val	His	Asp	Ile	Pro	Gly	Leu
			20					25					30		
Arg	Lys	Val	Ile	Gly	Gln	Lys	Val	Pro	Cys	Val	Ala	Val	Thr	Gly	Ser
		35					40					45			
Glu	Lys	Val	Leu	His	Lys	Lys	Asp	Tyr	Trp	Asp	Leu	Ala	Thr	Pro	Met
	50					55					60				
Pro	Ile	Ala	Trp	Gly	Thr	Thr	Asp	Arg	Thr	Val	Ile	Ala	Asp	Ala	Arg
65					70				75					80	
Arg	Thr	Ile	Pro	Thr	Thr	Glu	Trp	Asp	Ile	Leu	Ala	Arg	Leu	Arg	Pro
			85					90					95		
Arg	Leu	Glu	Glu	Val	Arg	Lys	Gln	Arg	Asn	Asp	Val	Leu	Leu	Leu	Asn
			100					105					110		
Glu	Glu	Asp	Pro	Pro											
			115												

<210> 149

<211> 407

<212> DNA

<213> Homo sapiens

<400> 149

nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gaccattttt
 60
 cctaatatgg ccgctcagat ccaatacttt gaagattcgt ccgtgggttat atggcacgat
 120
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 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
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 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
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 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
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<400> 156

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 35 40 45
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<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	
			565						570					575		
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	
		580						585					590			
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	
	595						600									

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
705	710	715
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		
	725	730
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn		735
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		750
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		765
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		780
785	790	795
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		815
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		830
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		845
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		860
865	870	875
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		880
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		895
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		910
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		925
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		940
945	950	955
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		960
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		975
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		990
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		1005
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		1020
1025	1030	1035
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		1040
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		1055
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		1070
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		1085
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		1100
1105	1110	1115
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		1120

	1125		1130		1135
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val					
	1140		1145		1150
Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly					
	1155		1160		1165
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu					
	1170		1175		1180
Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala					
1185	1190		1195		1200
Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe					
	1205		1210		1215
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys					
	1220		1225		1230
Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe					
	1235		1240		1245
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser					
	1250		1255		1260
Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr					
1265	1270		1275		1280
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg					
	1285		1290		1295
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met					
	1300		1305		1310
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr					
	1315		1320		1325
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu					
	1330		1335		1340
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg					
1345	1350		1355		1360
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly					
	1365		1370		1375
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys					
	1380		1385		1390
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr					
	1395		1400		1405
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val					
	1410		1415		1420
Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys					
1425	1430		1435		1440
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly					
	1445		1450		1455
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg					
	1460		1465		1470
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe					
	1475		1480		1485
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys					
	1490		1495		1500
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu					
1505	1510		1515		1520
Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu					
	1525		1530		1535
Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala					
	1540		1545		1550
Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser					

1555
Ser Ser Val Val
1570

1560

1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
gccggctctg ccatgtgctt actctgagcc acctaacctc ggcgtgcttc agtttactca
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tccgctcatc tgcagaatgg gtgatgctgt cggctacttcg tggcatacag gaaagtgtccc
120
agcatgggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc
180
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttggggtg ggacttccca aagggtcatgg aaaagttccc agtcaatgag atccatggag
300
acccatggga gtgggggtca gccccagcct aagaggaccc ccagccctgc cctgtgcccc
360
aggacacacc aggcactgtc ccttgctcgc ttcccagaca acctgtaccc tccaggccac
420
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgtcca gaggtgcac
480
gcttccctgc cccttccggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
1 5 10 15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
85 90 95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161
 nnacgcgtac gtcttttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc
 60
 cgcgcttggc tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc
 120
 gcccgggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg
 180
 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
 240
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc
 300
 aagacggtgc atgcgtactt tgggtgctgag acgtgcatgc atctgacgtg c
 351

<210> 162
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 162
 Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser
 1 5 10 15
 Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
 20 25 30
 Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
 35 40 45
 Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
 50 55 60
 Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
 65 70 75 80
 Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
 85 90 95
 Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
 100 105 110
 Met His Leu Thr Cys
 115

<210> 163
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 163
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 60
 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatactcc gttcaacttc
 120
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg
 180
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa
 240
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttggtacc
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10					15	
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35				40						45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65				70						75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
			85					90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
		100						105					110		
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
		115					120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

gctagcagcc ttcaccctcc tagaggggca ggctcggcga caaggggcgg ggggtgccccg
60
tcccagcgag ggacgcccgg ggctgggggt gccggtcgag cccggggcaa cagcttcacc
120
aagtttgga accgcaacgt cttcatgaag gacaacagct cttcttcag cacagactcc
180
cgctcccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca
240
gactccgaca gctcctactc agggaatgag tgtcaccctg tgggccgcag gaaccgccc
300
cctaagggcc ggggcggtcg aggggcccac atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gcccaccaag cgcagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga
480
cactcccgcc gcctgcgcct cgagcccctg gtgctgcaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgcccccgac ccgtccaccg tgcgccctgt ggcattccct
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
 1 5 10 15
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
 65 70 75 80
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
 85 90 95
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
 100 105 110
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
 195 200 205
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
 210 215 220
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
 225 230 235 240
 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 167
 nnacgcgtgg aaccagaact caggcccgtg tgaggagtct ggtttggaaac acacggggcc
 60
 gcaacacaga attgtcaggt cctgtgccgt gaccaccaac cctcggggcca tgccaggtgc
 120

tgggtgagggg caggtgggtc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
 180
 gtcctcatgg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc
 240
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg
 300
 ggcgtgcgga tcccgcggca ccagggggcc ggcattggtg tcctcacatg gctgagcctg
 360
 ctgcgcggcg ccgggcaggc caacgtgtgc gacgtgggtca ccagcacggg gtgcctggcg
 420
 gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
 480
 cccacggagc tgctggtcat cgtgggtggc
 510

<210> 168
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 168
 Gly Ala Gly Gly Ser Arg Gln Ala Pro Ala Gly Leu Thr Ala Leu Arg
 1 5 10 15
 Pro Gln Val Leu Met Gly Val Leu Arg Leu Gly Phe Val Ser Ala Tyr
 20 25 30
 Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr
 35 40 45
 Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg
 50 55 60
 His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg
 65 70 75 80
 Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys
 85 90 95
 Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His
 100 105 110
 Arg Leu Arg Val Pro Leu Pro Thr Glu Leu Leu Val Ile Val Val Ala
 115 120 125

<210> 169
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 169
 gaattccacc gcatgtcgtg tctggacgta tgtaggtcgc ggtagtgtgc gaccgccggt
 60
 gccttaaagg agagcgggca tcggcggttc agtacgagag gggaagggtg gcggatactt
 120
 attgtcgggtg cggcatcgtc catccacacc gttcgatggg tcaatggact ggtcaagcgg
 180
 ggtcacgagg ttcacctggc atcagtccat ccggcggggc gtcactccat tgatccccga
 240
 gtccggtacc acctggcccc acacggcggg aaggcaaaat acgtcgtcaa tgccggctgg
 300

ctgcgatcag tggcggctgg ggtgcaacct gacatcgtca acgtccacta tgcgaccggt
 360
 tatggtctgc tcgctcgtct tgcccatatt gacgccccga cgctgctgtc ggtgtgggga
 420
 agtgacgttt acgattcccc ccggggcaaat cccctcatgc gtcacatggt ccgatccaac
 480
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcgtgt cacgcgt
 537

<210> 170
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 170
 Cys Ala Thr Ala Gly Ala Leu Lys Glu Ser Gly His Arg Arg Cys Ser
 1 5 10 15
 Thr Arg Gly Glu Gly Val Arg Ile Leu Ile Val Gly Ala Ala Ser Ser
 20 25 30
 Ile His Thr Val Arg Trp Val Asn Gly Leu Val Lys Arg Gly His Glu
 35 40 45
 Val His Leu Ala Ser Val His Pro Ala Gly Arg His Ser Ile Asp Pro
 50 55 60
 Arg Val Arg Ile His Leu Ala Pro His Gly Gly Lys Ala Lys Tyr Val
 65 70 75 80
 Val Asn Ala Gly Trp Leu Arg Ser Val Ala Ala Gly Val Gln Pro Asp
 85 90 95
 Ile Val Asn Val His Tyr Ala Thr Gly Tyr Gly Leu Leu Ala Arg Leu
 100 105 110
 Ala His Ile Asp Ala Pro Thr Leu Leu Ser Val Trp Gly Ser Asp Val
 115 120 125
 Tyr Asp Ser Pro Arg Ala Asn Pro Leu Met Arg His Met Val Arg Ser
 130 135 140
 Asn Leu Val Ser Ala Thr Arg Ile Ala Ser Thr Ser His Cys Met Ala
 145 150 155 160
 Arg Val Thr Arg

<210> 171
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 171
 ctagacaagc tcgcgcgggt gggcttcgac actcttggtc tacagacctt cctaactgcg
 60
 ggggagaagg agtcccgcgc atggacgatt cacaagggcg acaccgcccc tgaggctgct
 120
 ggcgtcatcc ataccgactt ccagaagggg ttcacatcaagg cccaggtggt gtccttcggc
 180
 gaccttggtg aatttggcgg cgaaaaggag gccacaggctg ctgggaagct gcggttgag
 240
 ggcaaggagt acgttatgca ggacgggtgac gtagtggaat tccgatttaa cgtgtagctc
 300

tggtttgata cttacttggc ttaaccgcat ctgagatccg tcatatcttt ggcgtagcct
 360
 tattggtatg aataacatgc cgtagccaaa g
 391

<210> 172
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 172
 Leu Asp Lys Leu Ala Arg Val Gly Phe Asp Thr Leu Gly Leu Gln Thr
 1 5 10 15
 Phe Leu Thr Ala Gly Glu Lys Glu Ser Arg Ala Trp Thr Ile His Lys
 20 25 30
 Gly Asp Thr Ala Pro Glu Ala Ala Gly Val Ile His Thr Asp Phe Gln
 35 40 45
 Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu
 50 55 60
 Phe Gly Gly Glu Lys Glu Ala Gln Ala Ala Gly Lys Leu Arg Leu Glu
 65 70 75 80
 Gly Lys Glu Tyr Val Met Gln Asp Gly Asp Val Val Glu Phe Arg Phe
 85 90 95
 Asn Val

<210> 173
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 173
 ccatggagtg tcccttgtgc gagcattttg agagctatac caacacccat ccctgcaggt
 60
 cccagagccg agccatttct caggagagca ggaagggagc aggccgaggg gtgctcccag
 120
 ccagccccgg aaccgaggt ctggggacgc agccgaccag ccctccttgt ctgggcctct
 180
 gtttcctctt cgacacaggg aagcagggag gggccgatca gcgacttagg cctgttggct
 240
 gtggtgggggt cccctgcgtt tctgggaage cacggaccct gggatgtacc tgggtttcat
 300
 tcgcagtga
 309

<210> 174
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Glu Cys Pro Leu Cys Glu His Phe Glu Ser Tyr Thr Asn Thr His
 1 5 10 15
 Pro Cys Arg Ser Gln Ser Arg Ala Ile Ser Gln Glu Ser Arg Lys Gly

	20		25		30										
Ala	Gly	Arg	Gly	Val	Leu	Pro	Ala	Ser	Pro	Gly	Thr	Arg	Gly	Leu	Gly
	35		40		45										
Thr	Gln	Pro	Thr	Ser	Pro	Pro	Cys	Leu	Gly	Leu	Cys	Phe	Leu	Phe	Asp
50			55		60										
Thr	Gly	Lys	Gln	Gly	Gly	Ala	Asp	Gln	Arg	Leu	Arg	Pro	Val	Gly	Cys
65			70		75									80	
Gly	Gly	Val	Pro	Cys	Val	Ser	Gly	Lys	Pro	Arg	Thr	Leu	Gly	Cys	Thr
		85		90		95									
Trp	Val	Ser	Phe	Ala	Val										
	100														

<210> 175

<211> 8484

<212> DNA

<213> Homo sapiens

<400> 175

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nnactttttt tttttttttt catttatgct atggagaaac cagcatggag atgtcatggg
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agagcatgca caggccccgc cctagggagt ggtgatgtgt ttggggagggt gcttgtttcc
120
aggccatcc cacacgttgt ccagttggat cctatggcag gctggctgtg gctttctctc
180
tcttgcttct ctctctctc cagataaggg tctgcaggat cttctgctta gcaagtgggtg
240
gccaaaggact ggtggatggg tggctggaag cagcgcacat gctccacagt ggaactgtct
300
gtctccacgg acttcatgta tttgttcagg atggcaaaaa cctcattgtt caagatctga
360
tacttctga tccggtcggc catcttcttc aggggcacat tcttaatgat ttcctcttc
420
ccgtcctgcc tctgcacttt tagcagggtg taacagaagt cgaacaggtc aaagcgacgc
480
tgctggccca gcaggacaat gatggagcaa ccagcccagt tcaagccatc gccgaaacac
540
tgctcagctg tgaactcgtt ggttcccaca gggatgcagt acacgaactg catggcgctc
600
cacagccggt ggaactccac aactcatcg acgtgcatga cgccattggt gggcggtggg
660
ccccgccaga tggggctctg caggtagctc cgaatgcggg tcaggatgac ctcaaacatg
720
gacaggccac agcacagccg ctcttggtc aggaggtcac cctcgcgagc aatggcgatt
780
tgctgagggg tccccagccg ctcgatcaga gggaccagggt ggagcggggc atacttggtc
840
tccagacgtt tcattttggc atcaagtctc tccccctctt tcacatggac tcgcggcaag
900
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960
ctcgatgagg aggcagaaga ggatggcatt gccacttcc ctcaggctct ggaagcacgt
1020
ctgttttgag ctctgcgtac tcaatgatgt ccttcagctg gtggtggaag aactccagga
1080

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tccctgggga gccatactca tgtcggggca agcggcatat cttgggcata acctctatca
1140
gtgttttcac atactggaga atggttcctt ggagcaagct cttcacaatc tttagcagtt
1200
cctccatgac cacagcgatg ccctgataac ccaggagtct gcagatagtc ttgaaagtgt
1260
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1320
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1380
gaaaatggta aactgtccg aacaaaccgg ttggtagagc cgttgtagca gtagttgggc
1440
aggaagtcac agttgagctc ccagaagacg tgcagggtga tcctcccgta gggcgctgac
1500
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1560
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<212> PRT

<213> Homo sapiens

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Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Pro Ser Ser Ile		
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Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp Arg Asn Ala Phe		
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Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser		
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 <213> Homo sapiens

<400> 178
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala
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 Arg Ile Leu Glu Thr Asp Pro Ala Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
 100 105 110
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
 115 120 125
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
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<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 179
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 120
 ccattgggcc gggcagcccg aatccaaaat gtcggggcac gccagtgagg agtatggtaa
 180
 ggggccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga gcgcctgggt
 240
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga
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 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt
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 aa
 362

<210> 180
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 180
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 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
 20 25 30
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
 35 40 45
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
 65 70 75 80
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
 85 90 95
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
 100 105

<210> 181
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 181
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 120
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa
 180
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacggtgc cctgtacatg
 240
 gcctattccg ggcgtgtttt gttgtccggc tatatgaaca agcgcgatgc caaccaa
 297

<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

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Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
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Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
          20           25           30
Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile
          35           40           45
Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
          50           55           60
Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
65           70           75           80
Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
          85           90           95
Ala Asn Gln

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<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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120
aagcgcattct ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag
180
gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc
240
gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaacac cgatttcggc
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351

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<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

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Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
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Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
          20           25           30
Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
          35           40           45
Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
          50           55           60
Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
65           70           75           80
Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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	85		90		95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala					
	100		105		110
Asn His Phe Gly Asp					
	115				

<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 185
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 120
 gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
 180
 gtcattgctt tggtcataat gtgcttaact ggcgcagtag gtcattggaat ctggctgagc
 240
 aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca
 300
 ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
 360
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 396

<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 186
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile
 1 5 10 15
 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
 20 25 30
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
 35 40 45
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
 50 55 60
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
 65 70 75 80
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
 85 90 95
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
 100 105 110
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
 115 120 125
 Ile Val Lys Leu
 130

<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

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120
gatgagcatc gtcgtttgct tggcacggtc ggcatcaag aggtcatcga ggctgctcgc
180
cgcgagatc gcagtattgc tgacgcggtg gaaactaacg gcacctcac ggcgcggacc
240
gacactccgt tgtccgagct cttcgtccg accagcaacg ccagggtgcc gttggccgtt
300
gtcgacgagg acttccacct catgggtgct atctctcggg tgaccctgct cgacgcgatg
360
tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttgagaga caccggaaag
420
ctt
423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
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			20					25					30		
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
		35					40					45			
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50					55					60				
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70				75						80	
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90						95	
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
	115					120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

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 120
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga
 180
 gcaagggtata tcaggctcag aaccaggaaa agcagggttt taccccagtg ccccatatag
 240
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct
 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
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 420
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 429

<210> 190
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 190
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 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr
 20 25 30
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His
 35 40 45
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
 50 55 60
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
 65 70 75 80
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
 85 90 95
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile
 100 105 110
 Ala Ala Arg Thr Val His Met Leu Val Asn His
 115 120

<210> 191
 <211> 4845
 <212> DNA
 <213> Homo sapiens

<400> 191
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 120
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 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
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 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaac
360
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtggggccctt tattgaccag
420
gtttacgtcc tgcaaagtta cgcagagggg tggaagaag ggacctggga agagaagggtg
480
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660
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720
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<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

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Ala	Val	Ser	Trp	Pro	Pro	Ala	Ser	Ala	Ser	Gly	Gln	Glu	Phe	Trp	Pro
			20					25					30		
Gly	Gln	Ser	Ala	Ala	Asp	Ile	Leu	Ser	Gly	Ala	Ala	Ser	Arg	Arg	Arg

		35					40				45				
Tyr	Leu	Leu	Tyr	Asp	Val	Asn	Pro	Pro	Glu	Gly	Phe	Asn	Leu	Arg	Arg
	50					55					60				
Asp	Val	Tyr	Ile	Arg	Ile	Ala	Ser	Leu	Leu	Lys	Thr	Leu	Leu	Lys	Thr
65					70					75					80
Glu	Glu	Trp	Val	Leu	Val	Leu	Pro	Pro	Trp	Gly	Arg	Leu	Tyr	His	Trp
				85					90					95	
Gln	Ser	Pro	Asp	Ile	His	Gln	Val	Arg	Ile	Pro	Trp	Ser	Glu	Phe	Phe
			100					105					110		
Asp	Leu	Pro	Ser	Leu	Asn	Lys	Asn	Ile	Pro	Val	Ile	Glu	Tyr	Glu	Gln
		115					120					125			
Phe	Ile	Ala	Glu	Ser	Gly	Gly	Pro	Phe	Ile	Asp	Gln	Val	Tyr	Val	Leu
	130					135					140				
Gln	Ser	Tyr	Ala	Glu	Gly	Trp	Lys	Glu	Gly	Thr	Trp	Glu	Glu	Lys	Val
145					150					155					160
Asp	Glu	Arg	Pro	Cys	Ile	Asp	Gln	Leu	Leu	Tyr	Ser	Gln	Asp	Lys	His
				165					170					175	
Glu	Tyr	Tyr	Arg	Gly	Trp	Phe	Trp	Gly	Tyr	Glu	Glu	Thr	Arg	Gly	Leu
			180					185					190		
Asn	Val	Ser	Cys	Leu	Ser	Val	Gln	Gly	Ser	Ala	Ser	Ile	Val	Ala	Pro
		195					200					205			
Leu	Leu	Leu	Arg	Asn	Thr	Ser	Ala	Arg	Ser	Val	Met	Leu	Asp	Arg	Ala
	210					215					220				
Glu	Asn	Leu	Leu	His	Asp	His	Tyr	Gly	Gly	Lys	Glu	Tyr	Trp	Asp	Thr
225					230					235					240
Arg	Arg	Ser	Met	Val	Phe	Ala	Arg	His	Leu	Arg	Glu	Val	Gly	Asp	Glu
				245					250					255	
Phe	Arg	Ser	Arg	His	Leu	Asn	Ser	Thr	Asp	Asp	Ala	Asp	Arg	Ile	Pro
			260					265					270		
Phe	Gln	Glu	Asp	Trp	Met	Lys	Met	Lys	Val	Lys	Leu	Gly	Ser	Ala	Leu
		275					280					285			
Gly	Gly	Pro	Tyr	Leu	Gly	Val	His	Leu	Arg	Arg	Lys	Asp	Phe	Ile	Trp
	290					295					300				
Gly	His	Arg	Gln	Asp	Val	Pro	Ser	Leu	Glu	Gly	Ala	Val	Arg	Lys	Ile
305					310					315					320
Arg	Ser	Leu	Met	Lys	Thr	His	Arg	Leu	Asp	Lys	Val	Phe	Val	Ala	Thr
				325					330					335	
Asp	Ala	Val	Arg	Lys	Glu	Tyr	Glu	Glu	Leu	Lys	Lys	Leu	Leu	Pro	Glu
		340						345					350		
Met	Val	Arg	Phe	Glu	Pro	Thr	Trp	Glu	Glu	Leu	Glu	Leu	Tyr	Lys	Asp
		355					360					365			
Gly	Gly	Val	Ala	Ile	Ile	Asp	Gln	Trp	Ile	Cys	Ala	His	Ala	Arg	Cys
	370					375					380				
Leu	Pro	Thr	Ser	Leu	Ser	Ala	Glu	Ser	Gly	Ser	Gly	Gly	Phe	Gln	Arg
385					390</										

<210> 193

<211> 350

<212> DNA

<213> Homo sapiens

<400> 193

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gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgcaccc gctggccgac
120
cgtgccagca tcagccccga ggaggtcaag ggcgagacca tggtgatgtt gggcacgggc
180
ccctggtttc cccggggcccg cgggtgggggt ttggcccggg tttggcgctt ttctccagcg
240
ccgttaaggg catacgccgc agtttcgagg gctcgtcgtt ggagaccatc aagcacatcg
300
tggttcggg catggcgtga cggtggtgcc gcagctgtcc gtgccgcgcg
350

<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
1				5				10						15	
Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25						30	
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50				55					60					
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70				75					80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85					90					95		
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
		100					105						110		
Val	Arg	Ala	Ala												
		115													

<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgtcgttga gtgggcccgtt
60
gaaatggttc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa
120
ccagaacttg gcgacgattt ggccgccgtc ctgctcgatt ctcacgggt tgctgtcatc
180
agcgagggat cgaactggct tgccctcgcta cccgtgatcg taggtcgcaa cacggaacag
240
tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
 360
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccggtcctg
 420
 ttcgacgcga tcgaatttga tcctgatata gcgacaacgg atgtgctgta cgatttcgcg
 480
 ttccctctga tggat
 495

<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
 Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val
 1 5 10 15
 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
 caagcaatgc ttgacgcagt tggtgaatac ttaccagcac cgactgatat tccagcaatc
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 aaaggtatca atccagatga aactgaaggt gaacgtcacg caagcgatga tgagccattc
 120
 tcttcattag cattcaaat tgcaactgac ccattcgtag gtaacttaac cttcttcctg
 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
 360
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 198
 Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp
 1 5 10 15
 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg
 20 25 30
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
 35 40 45
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
 50 55 60
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
 65 70 75 80
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
 85 90 95
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
 100 105 110
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
 115 120 125
 Leu Glu Arg Met Glu Phe
 130

<210> 199
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 199
 acgcgtgaag tcgtgcatag atcgggtgtga catagagaag cctccgaccc aagctgcgta
 60
 tatcgcacaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
 120
 caatagtga atccccgaga acccagctat ggaaggggtt ccagatgctc gaaggcctgt
 180
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
 240
 aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggt
 300
 gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct
 360
 tccctctctc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga
 420
 cggccctcc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct
 480
 cagcctgagc acagctccgc ttgtaca
 507

<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
 1 5 10 15
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggatg
 60
 tgtgcctgca ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtggtga
 120
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
 180
 ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct
 240
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
 300
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
 360
 gctggtaccg ggctagccgg tcttccaggt ctcgatctg gatgtggtag aactccttca
 420
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct
 480
 tgacttcaag ctcttgcct gccttgctca cactcttttt gggaggc
 527

<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1 5 10 15
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
 ngtgcaccgg tggatcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc
 60
 cgacccaagg gagttgtcgt caccacacc ggactcgaca gcttcgcact cgaccagcag
 120
 cgtcgattcc acgcagatca ccactctoga accctgcact tcgccacccc cagcttcgac
 180
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggg gatcgtcccg
 240
 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1 5 10 15
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
 nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
 60
 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agatttaatt
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
 115

<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
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 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nntccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat
 60
 attcaaggtt ccacgactcg cacctgcctt gccaatataa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg caccgcgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
 Gln Pro Glu Thr Pro Ala His Ala
 50 55

<210> 211
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 211
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgtttgg aggcaatgtc
 60
 cagctggcag ctcagaccct tgcacacccat ggaggaagcc tcccacccga cctgcagttc
 120
 tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct
 180
 agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt
 240
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
 300
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
 354

<210> 212
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 212
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
 1 5 10 15
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
 20 25 30
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
 35 40 45
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
 50 55 60
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
 65 70 75 80
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
 85 90 95
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
 100 105 110
 Xaa Lys Glu Gln Leu Ile
 115

<210> 213
 <211> 669
 <212> DNA
 <213> Homo sapiens

<400> 213
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tgttgcagtc tattggggaa
 60

gttgaacaaa acctggaagg gaaacaggtg tcatacactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta ccccaggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5					10					15	
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
			20					25					30		
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
			35				40					45			
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50					55				60					
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65					70				75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
				85					90					95	
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
			100					105						110	
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
		115					120					125			
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130					135					140				
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150					155					160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165					170					175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
		180					185				190				
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

	195		200		205									
Glu	Lys	Asp	Ala	Ser	Ser	Cys	Gln	Glu	Gln	Leu	Asp	Glu	Phe	Arg
	210					215					220			

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtagca gcccttgacg atgtgagcct ggctattaag
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 agagggtcca tctcagccgt tatcgggcac tccggagccg gcaaattccac cctgggtcgc
 120
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt
 420
 ggtattgccc gagcgttagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctagggtgta cggtcgtcgt catcacccac gagatggagg tcgtccgctc gattgcccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcccg ccaggtcttc
 660
 gtcatccac agtcagagac caccacgcgt ttcctggcga cgattatcgg ccagcaccg
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcgggtg ccagtcactc gttcgggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

65					70					75				80
Gln	Phe	Asn	Leu	Phe	Gly	Ser	Arg	Thr	Ile	Tyr	Asp	Asn	Val	Ala Tyr
				85					90					95
Pro	Leu	Lys	Leu	Ala	His	Trp	Lys	Lys	Ala	Asp	Glu	Lys	Lys	Arg Val
			100					105					110	
Thr	Glu	Leu	Leu	Ser	Phe	Val	Gly	Leu	Thr	Ser	Lys	Ala	Trp	Asp His
		115					120					125		
Pro	Asp	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Gly	Ile	Ala Arg
	130					135					140			
Ala	Leu	Ala	Thr	Lys	Pro	Ser	Ile	Leu	Leu	Ala	Asp	Glu	Ser	Thr Ser
145					150					155				160
Ala	Leu	Asp	Pro	Glu	Thr	Thr	Ala	Asp	Val	Leu	Ser	Leu	Leu	Lys Arg
			165					170					175	
Val	Asn	Ala	Glu	Leu	Gly	Val	Thr	Val	Val	Val	Ile	Thr	His	Glu Met
		180						185					190	
Glu	Val	Val	Arg	Ser	Ile	Ala	Gln	Gln	Val	Ser	Val	Leu	Ala	Ala Gly
	195						200					205		
His	Leu	Val	Glu	Ser	Gly	Ser	Ala	Arg	Gln	Val	Phe	Ala	His	Pro Gln
	210					215					220			
Ser	Glu	Thr	Thr	Gln	Arg	Phe	Leu	Ala	Thr	Ile	Ile	Gly	Gln	His Pro
225				230						235				240
Ser	Gly	Glu	Glu	Gln	Ala	Arg	Leu	Gln	Ser	Glu	Asn	Pro	Asp	Ala Arg
			245					250					255	
Leu	Val	Asp	Val	Ser	Ser	Val	Ala	Ser	His	Ser	Phe	Gly	Asp	Ala
		260						265					270	

<210> 217

<211> 500

<212> DNA

<213> Homo sapiens

<400> 217

nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
 60
 agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
 120
 ttctctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
 180
 ctgttcaacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
 240
 gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
 300
 gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
 360
 caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
 420
 ctgggcatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
 480
 tcaaggggcg tccagctagc
 500

<210> 218

<211> 166

<212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

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<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caaggctcgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcatacagg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgata ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggecca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
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361

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<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

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      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

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<210> 221
 <211> 401
 <212> DNA
 <213> Homo sapiens

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<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcataatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcggct ccagtgacca cccccccagg gcataccctc ctacagagca
240
ttccccaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcctggtga accagcatcc aggctgggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

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<210> 222
 <211> 124
 <212> PRT
 <213> Homo sapiens

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<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
      1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120
 <210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens
 <400> 223
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 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtgggtgctt ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtcc
 240
 aaaagctggt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
 300
 gcaagggcac ttcccggggc ttccctgttc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttcattcgca cctccacctc
 60
 cagaatgacc ctcatccctt cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaacc
 300
 tttgctcaca ctggccctc ttcttggaac atgggcctn
 339

<210> 226
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Thr Leu Ile Pro Ser Cys Thr Asp Gly Asp Ser Ser Asn Ser Tyr
 1 5 10 15
 Lys His His Gln Thr Asp Leu Gln Glu Gln Arg Asn Ser Gln Ser Arg
 20 25 30
 Phe His Pro Arg Arg Ala Leu Lys Ser Ser Arg Ala Ala Cys Tyr Gly
 35 40 45
 Gly Gly Arg His Thr Leu Leu Gly Ser Gln Gly Leu Ser Gln Pro Gly
 50 55 60
 Pro Asn Gln Leu Pro Ala Trp Pro His His Pro Thr Ala Lys Pro Leu
 65 70 75 80
 Leu Thr Leu Ala Pro Leu Pro Gly Thr Trp Ala
 85 90

<210> 227
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 227
 gtcgaccct tcgattgtgg cgaactccat ggctgctgcg ggcctgcgta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
 180
 ggccaggccg acaagtgctg cctcctgcca cccgctgagc gacgctgcca tgttgagtac
 240
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
 353

<210> 228
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 228
 Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1	5	10	15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly			
20	25	30	
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu			
35	40	45	
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro			
50	55	60	
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val			
65	70	75	80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala			
85	90	95	
Thr Ile Glu Gly Val Asp			
100			

<210> 229
 <211> 743
 <212> DNA
 <213> Homo sapiens

<400> 229
 nnggctaggg acacggcctc ctctcaaca ggcagtgcct gtgcaggctc aggggcatca
 60
 tcaaagataa cacagggtg gtcaggggct gctggctgct cctgccccag gactggctcc
 120
 aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccaggag
 180
 tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
 240
 agtaaagtgt ctgccccagg ggtgctcaca gccaggacc gggtagttgg aaagccagcc
 300
 cagcttggca ctgagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
 360
 gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaag
 420
 agagattcac tgggtacctc cagtagtcga gatgtaagcc ttggggactg ggaatttggg
 480
 aagagagatt ctctgggtgc ttatgccagc caagatgcc aagagcagg ccaagatttg
 540
 gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
 600
 tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
 660
 caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
 720
 cttgacgccc aggacagaag ctt
 743

<210> 230
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 230
 Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

1	5	10	15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly			
20	25	30	
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu			
35	40	45	
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg			
50	55	60	
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln			
65	70	75	80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val			
85	90	95	
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val			
100	105	110	
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser			
115	120	125	
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu			
130	135	140	
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly			
145	150	155	160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln			
165	170	175	
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln			
180	185	190	
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu			
195	200	205	
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly			
210	215	220	
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr			
225	230	235	240
Leu Asp Ala Gln Asp Arg Ser			
245			

<210> 231

<211> 431

<212> DNA

<213> Homo sapiens

<400> 231

acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcaggggtcc
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caggggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
180
tctcgctgga ggccaggagg atgatggtgc tggctgtgtc cttgtccagc tcaactggcgc
240
gactgctcag gaccctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgagc caggagcgt ctccaccctg ctggacgcca
360
tcaccgataa ggacccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
420
aggtgcggcc g
431

<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
 60
 aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagcttct
 120
 gtgctggaat gcacccccat cggaaaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc
 420
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggctgcc cagctcctac tctgcctctg cactcactg actgtgtggt
 540
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt
 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1 5 10 15
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
 cgaccgttga ctattctcta caaaccacaa agacaatgat tgatttaact gaatttagaa
 60
 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattcctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag
 180
 aaagaggaaa aagaaggga acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65		70		75		80									
Leu	Asp	Leu	Leu	Ser	Leu	Lys	Asn	Met	Ser	Glu	Ala	Gln	Ser	Lys	Asn
				85				90						95	
Glu															

<210> 237
 <211> 2059
 <212> DNA
 <213> Homo sapiens

<400> 237
 ggccataagg gcacgacgca ttcctagccg atgcaccaac acgggcatga agcctgccga
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 gagcacgaag ccggcggtcca tagctacggc ccatacgggc atgtctgccca tggctccggt
 120
 gatgtcagac tgcacatgaa atcgggttacg gtaccccagg atcatcgcta ccgagtacac
 180
 cccgaacagc acccgctggg cgccgatcag cgtgaggag tgccccacca gtggcacttt
 240
 tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg
 300
 atccaccagt ggcggcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac
 360
 tgcgaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtggtgca caggaatatg
 420
 gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg
 480
 ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgtcgat ggtgtattcc
 540
 aaccacagcga ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaacca
 600
 atgagcaagg ccagggtggga gggcttatcg cgcgaccac ccagaccaa gatccccagc
 660
 ccgacccagg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc
 720
 tctctgatct gcagctcatc aagggttacg gactgcagta cctcaatgca ctctggcta
 780
 cccgagccca gaacctgcca cagtcccctg agaacaccga cctgcagggt attccaggca
 840
 gccagaccag gtccttggt gagaagacca ccacagcggc agctttccca gtagcccttt
 900
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 960
 ttgttttcag agcacacgta aggggtccagc cacagcaggc ccggcgctccc ggtggaaggc
 1020
 agccctgggc ggaacccagg cgtttaacgg ctactaggc agccccagat ctggggaagc
 1080
 agatgagcac gtggggagct ggagtgagct gagcagaagt tttgtgccc cctgccccca
 1140
 tcccctccag gccacgtttt agatggccct tgtagttgcg ggtcctgggt gtcctcagaa
 1200
 ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca
 1260

ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta
 1320
 gttcccaggg ccagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga
 1380
 ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg
 1440
 acctctatct gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca
 1500
 agccgagagc acccattttg gctggggatt cagatcgatg gccttgtcca tgttgctcctt
 1560
 tctggcttcc ctgatggtgt catgtttcag cgcattgcgc ccagcctttc ccatgtgcca
 1620
 aaccagaagc tccactgccc gtaggctgtc cctgtagecc tgctccctcc ctggaggctg
 1680
 ctcttctgat tctgagagct ggcctagtgg tgetgagggc ccctttctgc ttctctgccc
 1740
 acctgctgag ttgccactcg cagtgttgct agttcccgtg ttctgagaag aggtcatgcc
 1800
 tgggaggaag ggatcgatc gctgcatcga atcctctctc cgccgtgtgg ccccaggag
 1860
 agtagctgcc tgttgacact gctccacacc tccccacagc ctccctgcag gtgctgtgtg
 1920
 gccgtgatgt gcagagagca gtgagggagg gttcatgaac caggtggatc ctctttaaaa
 1980
 aaaaaaaaaa tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa
 2040
 agacttgaaa tgttctaga
 2059

<210> 238
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 238
 Ala Glu Gln Lys Phe Cys Ala Arg Leu Pro Pro Ser Pro Pro Gly His
 1 5 10 15
 Val Leu Asp Gly Pro Cys Ser Cys Gly Ser Trp Val Ser Ser Glu Leu
 20 25 30
 Asp Ile Asn Ala Trp Ile Leu Gln Pro Ala Leu Pro Ser Phe Arg Arg
 35 40 45
 Gln Glu Ser Pro Gly His Ser Pro Pro Gly Pro Pro Gln Glu Gly Met
 50 55 60
 Lys Gly Met Pro Ser Ser Leu Val Pro Arg Ala Gln Pro Ser Pro Ser
 65 70 75 80
 Pro Pro Gly Gln Gly Gln Cys Gly Ile Phe Arg Phe Arg Pro Leu Trp
 85 90 95
 Ala Glu Pro Pro Cys Glu Cys Ser Tyr Cys Leu Cys Val Ala Val Thr
 100 105 110
 Ser Ile Cys Leu Leu Leu Ile Cys Gln Pro Ile Ala Ala Gly Ser Thr
 115 120 125
 Phe

<210> 239
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 239
 ntctagatca ctctgtagcg catgggttaa tgctgacaca atagaaaagt gcgaggacat
 60
 cctcgaatta atgagatggg ggactggatg agtcaagttc tcgtcgttgc ggcggctgtc
 120
 ggtcagctgc ccctcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg
 180
 tgttcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag
 240
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
 300
 cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tgggtacctat
 360
 ggtcgtgtat ataaagcaaa ggaacttn
 388

<210> 240
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 240
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
 1 5 10 15
 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
 20 25 30
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
 35 40 45
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
 50 55 60
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
 65 70 75 80
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
 85 90 95
 Arg Val Tyr Lys Ala Lys Glu Leu
 100

<210> 241
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 241
 ncggggggcc gagttgaaag ctgccggcac actggctgtg ctgcttgctt cacttctcgg
 60
 gatgctgctt ccagggcggg cctgggggaa acatcggcct tcccaggcac ccttagcccg
 120
 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat
 180

gtgggcaaac tgggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt
 240
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat
 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
 1 5 10 15
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
 20 25 30
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
 35 40 45
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
 50 55 60
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
 65 70 75 80
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
 85 90 95
 Ser Ala Pro Arg
 100

<210> 243
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 243
 nnaccttctc tccgcgttat taccaaagat gctatgcacg taactgcgga ggaaattctt
 60
 cacacaggcc accccgcccc cactgcgctc gtcgctaate ttccctataa cgttgcggtg
 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatgggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cgggtgtcccc
 240
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc
 300
 ttctggccgg ctcccaatgt tgattctggn
 330

<210> 244
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 244
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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      1           5           10           15
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      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
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<210> 245

<211> 355

<212> DNA

<213> Homo sapiens

<400> 245

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Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
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Lys Leu Gly Gly Gly
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<210> 247
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 <212> DNA
 <213> Homo sapiens

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 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
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<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
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Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
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		340					345						350		
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Ile	Val	Cys	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val
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<211> 291

<212> DNA

<213> Homo sapiens

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<211> 97

<212> PRT

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Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
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Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
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Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
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300
acgacttcgg acggcgactc gacgcgt
327

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<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

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<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
      1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
      65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100           105

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<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatccc tgttatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgcggacacc atgcccgaac ccggcctgct cgccatcgag
 60
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
 120

cgggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
 180
 ttcgggtcgag ttcgggaatg gctggacgct gtgccagcca aggacccgtc aagcatttcc
 240
 ctggctcact cgaaagctgg actcaacgag gagtaccagc agtcatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtggttct tgggcccga ggcgcgcgatc ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg
 480
 agcaaggctc tcattcattga tgagggtccac gccgccgacg tctatatgcg cgaatacctc
 540
 aaggctcgtcc tcgaatggct cggcgcctac cgcacgccag tcactctcat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcgcg ctagcgtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65					70					75				80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
			85					90						95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
	115						120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145					150					155				160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
			165					170						175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
	180							185					190		
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
	195						200					205			
Leu	Ala	Leu	Ala	Tyr											
210															

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatggtgtg tgcacgtgtg cnaactgtgta tgcattggtaa tgtgcacgtg tgcactgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgt
 240
 atgcaatggt gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccggt tcgcgttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcggg
 60
 ctgtggggcg gcatcgctctt cggatcgctg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggttggtat tccgatcttt tccgaagatc cgtcgtgggc ctcggctact
 180
 ggcacggtct accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct
 240
 gttagcccggt acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccctc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttegtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
 720
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac
 960
 cgatcgctct gatgaccgcg atcttcctag tcgagtagcg ccgcggaact aagatcgcca
 1020
 aggtcattag cttegccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggccctcat gatcctcatg gtcccgacgg tgctgcgac aaccgaggaa atgctcaagc
 1200
 tt
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10					15		
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
			20					25					30		
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
		35					40					45			
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
	50					55				60					
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65				70						75				80	
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
			85					90				95			
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
		100					105					110			
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
	115					120						125			
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

130 135 140
 Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
 145 150 155 160
 Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
 165 170 175
 Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
 180 185 190
 Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
 195 200 205
 Ala Lys Gly Val Lys Arg
 210

<210> 263
 <211> 424
 <212> DNA
 <213> Homo sapiens

<400> 263
 acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
 60
 gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacggt
 120
 gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
 180
 tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
 240
 gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
 300
 caggccccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
 360
 gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
 420
 gann
 424

<210> 264
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
 1 5 10 15
 Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
 20 25 30
 Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
 35 40 45
 Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
 50 55 60
 Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
 65 70 75 80
 Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
 85 90 95
 Lys His Xaa

<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact ccctcatcgg caagctcatc atcactgggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc
 180
 tttcaccagg cggtgggttca cgacccggct ttcactgccg ccgacggctg cttcggcgctc
 240
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtcaa cggtaaacgc
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg ccgggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttcg aagctcgca ttaccgccag attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcc a tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgtggc atggatacga accctgctcg ctgagttcag cagaatcacc
 420
 tcacacttca catttttgtc atgggtaggc catcactgtg atgatgccg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35					40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85						90				95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
		100						105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115				120						125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145				150							155				

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
 120
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tgttcggttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccgggcggtc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tgggtcaaact actacgc
 387

<210> 270
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 270
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
 1 5 10 15
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
 20 25 30
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
 35 40 45
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
 50 55 60
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
 65 70 75 80
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
 85 90 95
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
 100 105 110
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
 115 120 125
 Arg

<210> 271
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 271
 gccggcacca acggaaagtc ctctaccgcg cgcattggctg attcgctttt gcgtgccttc
 60
 caccgcccag tgggttttgg aaccagccca cacctgcagc gcgttactga gcgcattcggc
 120
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtgaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtccga ggtcttcgtg
 240
 ggctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctgctcccc cctgctgtcg
 60
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
 180
 tgctgcctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
 240
 catttcctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcca cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgtca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274

<211> 116

<212> PRT

<213> Homo sapiens

<400> 274

Met	Trp	Thr	Gly	Arg	Glu	Val	Ala	Trp	Pro	Gln	Asn	Ser	Ile	Lys	Glu
1				5					10					15	
Lys	Leu	Leu	Glu	Glu	His	Asp	Trp	Phe	Trp	Ala	Gly	Lys	His	His	Pro
			20					25					30		
Arg	Ser	Gly	Asn	Ala	Val	Ser	Arg	Glu	Pro	His	Gly	Met	Arg	Thr	Pro
			35				40					45			
Ala	Gly	Gly	Gln	Phe	Ser	Gly	Ser	Ser	Cys	Leu	Arg	His	Ser	Val	Leu
			50			55					60				
Gln	Gly	Gly	Gln	Asp	Pro	Tyr	Trp	Asp	Pro	Gly	Ser	Glu	Val	Gly	Met
65				70				75						80	
Pro	Asp	Phe	Arg	Ala	Phe	Glu	Val	Gly	Gly	Gly	Gly	Phe	Gly	Phe	Ser
			85					90						95	
Ser	Thr	Ala	Gly	Gly	Ser	Glu	Leu	Gln	Ser	Arg	Thr	Gln	Asn	Leu	Lys
			100					105						110	
Gln	Ser	Tyr	Phe												
			115												

<210> 275

<211> 911

<212> DNA

<213> Homo sapiens

<400> 275

naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
 60
 ttattttcag gaatgaaagg aattaccag ccttctgctt ttatacctac agctgaaagt
 120
 aattcctttc agctcaggt gaagactttg ccattctcaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtcct
 360
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctgggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtgggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
1				5					10					15	
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
			35				40					45			
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
			50			55					60				
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65					70					75					80
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
				85					90					95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
			100					105					110		
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
			115				120					125			
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
	130					135					140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145					150					155					160
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
				165					170					175	
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
		180						185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
		195					200					205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
	210					215					220				
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile

```

225          230          235          240
Lys Asn Gly Ser Val Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser
                245          250          255
Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr
                260          265          270
Ser Ser Asp Glu His Pro Val
                275

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<210> 277
<211> 652
<212> DNA
<213> Homo sapiens
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<400> 277
nnaccggtgg ggactctcgc tgaggtcctt aatggccctt ctcgtgtccc ggacggcacc
60
atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa
120
gagttccagc gcatcgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc
180
ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg
240
ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaagggtc
300
cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc
360
gcccgtaggg ctgagcagat cgcgcggttg cggcagttag cggtcagatc gaacctcgac
420
cccgaattcg cgcagaaggc catcacgttc atcgtggccg aggtgggtgcg tcaccacgaa
480
gctattgctg acgattctgg cgacgactct ggagtggcgg atacggggga ggcggatgtc
540
cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccttcgac
600
gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt
652
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<210> 278
<211> 115
<212> PRT
<213> Homo sapiens
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<400> 278
Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp
 1          5          10          15
Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile
      20          25          30
Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala
      35          40          45
Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala
      50          55          60
Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe
65          70          75          80
Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

```

85 90 95
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
 100 105 110
 Ser Gly Ser
 115

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 279
 cgggaggtca cacaagcatt caaaccatag cagatggtaa atgttatgtt atgtgtattt
 60
 taccacaatc cttaaaaaga aaagaaagaa aggcataatgg aacccttagt tacctctcat
 120
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt
 180
 ttccagaaaag aagaccacaga ggattccaca tctgcctgga aaccacgacc agtctcgact
 240
 ggaagtgtgt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
 300
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
 348

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
 1 5 10 15
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
 20 25 30
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
 35 40 45
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
 50 55 60
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
 65 70 75 80
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
 85 90 95
 Pro Lys Ile

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 281
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac
 60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
120
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
180
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
240
gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
300
caaaaacagg ccaggaatct cgtgtcagtg aacggtagcc tgcagaaccc caacgggtgat
360
tctgtcatta agattcaaca gacc
384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1				5					10					15	
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20						25					30		
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
		35						40					45		
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55					60				
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65					70					75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
				85						90				95	
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
				100						105				110	

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

cgcgtagacc aatgtgagac ggccgtcacc aagggcatgc gcgacaagtc ggttggttagc
60
ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
120
ggaagcgtac tggtcgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
180
tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
240
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
300
cgcacaaagg aagtcttgca tgaaaaaggg gtcattgtgc cttccacgct gcgcttgatc
360
cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgattttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcgtgcggt tgtttgcaca accctgggggt tataacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn			
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu			
	35	40	45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly			
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu			
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile			
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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nnttaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttgct
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tcagttgagg gattcgggac aatagcagtg ctgatggtaa tgttggcgat tccctgttt
120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttccagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg cccagctgg ggccgcctgc ctggagagat ccaggagcgt ggccctgccc
900
tcttgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

```

ggtgacctta aaactgacta cacccttttc acaggggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcctc cagcgcttgt
 1200
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgcag
 1320
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35					40					45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70					75				80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
				85					90					95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115					120					125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
		130				135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145					150					155				160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
				165					170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185					190			
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195					200					205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215					220				
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225					230					235				240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
				245					250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260					265					270			
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

275	280	285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp		
290	295	300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		
305	310	315
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe		
325	330	335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys		
340	345	350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		
355	360	365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		
370	375	380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly		
385	390	395
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu		
405	410	415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		
420	425	

<210> 289

<211> 822

<212> DNA

<213> Homo sapiens

<400> 289

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ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catgggtgat
120
agcaagtcca aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
accctgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccggt gattttgtgc agggtagatt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgtaccg ctcgtcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

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<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacggggcgt cgctgccggg ctgagtgccg ggcccgcctcc
 60
 atcaccccc gcacgcctcg ccgcggcgtg gagaccagcg agcgcttggg ccggtatcgc
 120
 tgggtcgctg agcgcacctt cgccctggctc aaccgctttc ggcgccctgc catccgctac
 180
 gagcggcgtg ctgacatcca cgaagccttc gtgatacctg gctgcgccct catctgcctc
 240
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

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Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
      20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
      35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
      50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
      85

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<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

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nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcattgtg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaaggtt
240
gcgaagactt tcgatgttcc agtgtgctgc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgatttgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgtact cgccgatctg
420
ggggttgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgccggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccgggtga gtgattctcg tttctcgatg
540
gtggcgggaga cgacccatcg cattggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaagggtctca aatgtgccga ctgatcaata cgcattccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

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<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

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Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

1	5	10	15
Thr Ala Asp	Ala Ile Leu Ala Ala	Leu Asp Leu Asn Arg	Phe Lys Val
20	25	30	
Ala Lys Thr	Phe Asp Val Pro Val	Cys Val Ile Ala Gly	Ala Gly Thr
35	40	45	
Gly Lys Thr	Arg Ala Val Thr His	Arg Ile Ala Tyr Gly	Ala Ala Thr
50	55	60	
Gly Lys Leu	Asp Pro Arg Arg Thr	Leu Ala Val Thr Phe	Thr Thr Lys
65	70	75	80
Ala Ala Gly	Thr Met Arg Gly Arg	Leu Ala Asp Leu Gly	Val Val Gly
85	90	95	
Val Gln Ala	Arg Thr Ile His Ser	Ala Ala Leu Arg Gln	Ile Lys Phe
100	105	110	
Phe Trp Pro	Arg Ala Tyr Asn Cys	Glu Leu Pro Pro Val	Ser Asp Ser
115	120	125	
Arg Phe Ser	Met Val Ala Glu Thr	Thr His Arg Ile Gly	Leu Gly Asn
130	135	140	
Asp Lys Ala	Leu Leu Arg Asp Leu	Ser Ala Glu Ile Ser	Trp Ala Lys
145	150	155	160
Val Ser Asn	Val Pro Thr Asp Gln	Tyr Ala Ser Leu Ala	Arg Ala Glu
165	170	175	
Gly Arg Val	Val Ala Gly Val Ser	Ala Thr Asp Val Gly	Arg
180	185	190	

<210> 295

<211> 417

<212> DNA

<213> Homo sapiens

<400> 295

ttcatatcag gcagtaaccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
 60
 tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
 120
 ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
 180
 gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
 240
 gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
 300
 cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
 360
 atcgagtcat tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
 417

<210> 296

<211> 139

<212> PRT

<213> Homo sapiens

<400> 296

Phe Ile Ser	Gly Ser Thr	Arg Val His	Ala Ile Asn	Asn Val Ser	Val
1	5	10	15		
Ser Phe Thr	His Ser Gly	Val His Leu	Leu Met Gly	Glu Ser Gly	Ser

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

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<210> 297
 <211> 378
 <212> DNA
 <213> Homo sapiens

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<400> 297
tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccgaggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcgtaa tgatcaccca cgacctcggg gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

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<210> 298
 <211> 126
 <212> PRT
 <213> Homo sapiens

```

<400> 298
Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50      55      60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

	85		90		95
Glu Thr His	Ala Gly Val Val Met	Ile Thr His Asp Leu Gly Val Val			
	100	105	110		
Ala Gly Leu	Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg				
	115	120	125		

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 299
 gtgcacggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
 60
 ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcggt
 120
 ttcctggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
 180
 gtgcgcggtg agctctacca cattgggggtt gagccggtga gggtgccgtt gtccgatcag
 240
 gggccgttgc gtccctagcct gcgcggttacc catccgatct cgggggttgcg tcgagctgac
 300
 ggttctctta tcactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
 360
 atctcgac
 368

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe															
1	5	10	15												
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu															
	20	25	30												
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr															
	35	40	45												
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu															
	50	55	60												
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln															
65	70	75	80												
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu															
	85	90	95												
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile															
	100	105	110												
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser															
	115	120													

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301

ggccgggtta ttgcccgccc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc
60
aacggcgcg actattccgt accgccgccc gaaccgacct tgctcgacag gcttacggac
120
gcgggccgga cggatgatgc aatcggcaag attggtgata tctacgcgca caaaggcgtg
180
tctcaggtgc gtaaggcaat ggcaatattg gccttggttcg atgaaacact cattgccatg
240
gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
300
gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggctg
360
ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcttgacagc cgatcatggc
420
tgcgaccgga ccctcaaggg aaccgaccac acgcgt
456

<210> 302

<211> 152

<212> PRT

<213> Homo sapiens

<400> 302

Gly	Arg	Val	Ile	Ala	Arg	Pro	Phe	Val	Gly	Glu	Thr	Arg	Gln	Thr	Phe
1				5					10					15	
Glu	Arg	Thr	Gly	Asn	Arg	Arg	Asp	Tyr	Ser	Val	Pro	Pro	Pro	Glu	Pro
			20					25					30		
Thr	Leu	Leu	Asp	Arg	Leu	Thr	Asp	Ala	Gly	Arg	Thr	Val	Ile	Ala	Ile
			35				40					45			
Gly	Lys	Ile	Gly	Asp	Ile	Tyr	Ala	His	Lys	Gly	Val	Ser	Gln	Val	Arg
	50				55						60				
Lys	Ala	Met	Ala	Ile	Leu	Ala	Leu	Phe	Asp	Glu	Thr	Leu	Ile	Ala	Met
65					70					75				80	
Asp	Asp	Ala	Gln	Asp	Gly	Asp	Leu	Val	Phe	Thr	Asn	Phe	Val	Asp	Phe
			85					90					95		
Asp	Met	Leu	Tyr	Gly	His	Arg	Arg	Asp	Val	Pro	Gly	Tyr	Ala	Ala	Ala
			100					105					110		
Leu	Glu	Ala	Phe	Asp	Arg	Arg	Leu	Pro	Glu	Ala	Met	Ala	Lys	Leu	Arg
			115				120					125			
Thr	Gly	Asp	Leu	Leu	Ile	Leu	Thr	Ala	Asp	His	Gly	Cys	Asp	Pro	Thr
	130				135						140				
Leu	Lys	Gly	Thr	Asp	His	Thr	Arg								
145					150										

<210> 303

<211> 402

<212> DNA

<213> Homo sapiens

<400> 303

nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcatcgtcgc
60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc agggctctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg
 240
 atcggttaca acgcctgggc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga
 300
 gagatgggtc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgatc agatcgctcg ttaccggag agttatgtgc ac
 402

<210> 304
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Tyr Leu Gly Ala Gln Leu Phe Ser Asp Ser Glu Tyr Glu Gln Arg
 1 5 10 15
 Leu Arg Arg Val Arg Glu Leu Met Asp Arg Gln Gly Leu Ser Ala Ile
 20 25 30
 Ile Val Thr Asp Pro Ala Asn Ile Phe Tyr Leu Ile Gly Tyr Asn Ala
 35 40 45
 Trp Ser Phe Tyr Thr Pro Gln Met Leu Phe Val Pro Ile Asp Gly Glu
 50 55 60
 Met Val Leu Tyr Ala Arg Glu Met Asp Arg Met Ala His Ile Xaa Thr
 65 70 75 80
 Thr Ser Leu Pro Ala Asp Gln Ile Val Gly Tyr Pro Glu Ser Tyr Val
 85 90 95
 His

<210> 305
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 305
 nnacgcgtcg gttccgcac gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgtcgtcct ggcgaatatg ggcgatcagc cggtagctt cgggatcgtc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccg
 240
 tcgccatgcg tcggaatcga catgcagcac cctcctgcca ggatcgatgg cgtaatacgt
 300
 gcgacggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagtctctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcattcctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgcaca
 180
 tttgatgtct cttcttctca cccactcacc ccacctggg ggtaggggca aaaaagtggc
 240
 tcaaagctgc gggttcagagt tccttgtaaa caaggctcct cctcactgt cctcaccctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccga
 360
 gcagaactgg acataatggg aacaggggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgga
 480
 tggctcagcc tctggacatc accccaacca accagagccc tggctcttgc tggatgtcca
 540
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgatat ccctgtgcat atggctcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggtcg cgagccgatac
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgccagga gcagctgcat
 300
 gatgtcctcg ataccttgct cgagcgagag gccggtgtcg tgcgatgctg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggcaaag tctacgggtg tactcgggag
 420
 cgcacccgcc ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

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<210> 311
 <211> 358
 <212> DNA
 <213> Homo sapiens

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<400> 311
acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gaggggccg atgtggtggt cattggctct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

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<210> 312
 <211> 116
 <212> PRT
 <213> Homo sapiens

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<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

100 105 110
 Leu Val Lys Arg
 115
 <210> 313
 <211> 347
 <212> DNA
 <213> Homo sapiens
 <400> 313
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
 60
 acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc
 120
 agtggcaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
 180
 cgcctgggac tgcgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg
 240
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg
 300
 caagacgagg tggtcacggc ccccggcggc ttccatgtgc tgctagc
 347

<210> 314
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 314
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
 1 5 10 15
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
 20 25 30
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
 35 40 45
 Thr Phe Val Ser Ala Asn Leu Ala Ala Ala Leu Thr Arg Leu Gly Leu
 50 55 60
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
 65 70 75 80
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
 85 90 95
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
 100 105 110
 Val Leu Leu
 115

<210> 315
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 315
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggtcgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cggtgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcgc
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaacttc
 360
 cgccatgggc ccctgcccct gttcgtggca accctgtcga acccgaaggc gctgatcttc
 420
 gccagcgtga tctttcccgg caaggcggtc ctcgacttct ggaacaacta cacgatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggccc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagagggttt gtccactgag agaagcacat tggaaagggg ggcgtgggcc tgggactgtg
 120
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
 180
 ggggtgtggg taacatgccg tgcatttttg ggggtgtgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcattgtat catgtgggtg tggcgcagca aactcagctc ttacctggct
 300
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5					10					15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
			20					25					30		
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
			35				40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55				60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65				70						75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	
Leu	Leu														

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtacccctt ccgagcagtc ctattctcga gctgagcggg cacagtggcc
 60
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa
 240
 gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccggtg ctgcttata
 300
 cggccccgtc tatggtaaac aatgctagct ggctcggcat gcctgcgcca tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagtgag tggactgagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgcacgac gtgctcgcca agtcctcgg gtcctctaata gcgatcaacg tggttcacgc
 60
 caccgtcgat gcgttgcagc agctcgagga gcccgaagag gtcgcccgtc gccgcggcaa
 120
 gtccgttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggttaac tgatgagcaa gctgaagatc
 240
 acccagatca agtctggcat cgctaccaag ccaaatacgc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga cacggtcac aaggaggacc gcccgagatt ccgcggcatg
 360
 gtccggaccg ttcgtcacct cgtcaccatg gaagagggtg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgtc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

1	5	10	15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly			
	20	25	30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg			
	35	40	45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp			
50	55	60	

<210> 323
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 323
 ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
 60
 aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
 120
 gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
 180
 tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
 240
 ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
 300
 ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
 360
 gtgttctgtc cactttgcca ttaataccc gatgagaatc caagcagctt cagtggcagt
 420
 ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
 468

<210> 324
 <211> 156
 <212> PRT
 <213> Homo sapiens

1	5	10	15
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr			
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu			
	20	25	30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser			
	35	40	45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu			
	50	55	60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly			
65	70	75	80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe			
	85	90	95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr			
	100	105	110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu			
	115	120	125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His			

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggga tcccactcc cgcagatgac ttgcccgaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcacccactt ggttcactgt gtgcttccgg
 300
 gtcccaggt tttaggtgct tcatgcctg ctgggaacga gacacgtcc tgccctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttctatt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga ggggtgcgtga tgggctctgg
 120
 ggaatggagg atggcgcacc ggctgtgggt ggactgtgga aacgggggggt ggcagtgccg
 180
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaacca
 300
 ccctttaaca gtgcacaaag cgctggcaca cgggccacgt ctgggtgacgc aggctgcccg
 360
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgcccctgtc ccactctggc cagccggagt tttcaccta cagaccaata ggaaagaaca
 480
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgcc
 538

<210> 328
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Val Gly Ala Leu Arg Ala Ala Cys Val Thr Arg Arg Gly Pro Cys
 1 5 10 15
 Ala Ser Ala Leu Cys Thr Val Lys Gly Trp Val His Phe Thr Trp Pro
 20 25 30
 Leu Val Phe Ser Trp Val Ala Leu Ser Pro Ser Arg Ala Leu Leu Asp
 35 40 45
 Arg Ile Ser Pro Ala Gln Asp Pro Lys Thr Arg Pro Ala Gly Gln Leu
 50 55 60
 Pro Arg His Cys His Pro Pro Phe Pro Gln Ser Thr His Ser Arg Cys
 65 70 75 80
 Ala Ile Leu His Ser Pro Glu Pro Ile Thr His Pro Leu Tyr Gln Gln
 85 90 95
 Thr Thr Gly Arg Phe Ser Pro Ser Arg Ser Phe Ser Pro Asp Arg Pro
 100 105 110
 Ile Gly Lys Asn Thr Gly Pro Lys Leu Asp Phe Ile Val
 115 120 125

<210> 329
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 329
 tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt cttctgctc cactgagcag tgttttcctg atacccttg taccctgcca
 120
 gcagcctcgt tatgactcct aactccattg ccctccatgg ccctggggcg ctctctctct
 180
 cttctcttcc aggtagtaga gcactgcttc tggtctcttg tgcacagaag ggtttccac
 240

agctgagagc tgggctccta ctgacatagt tatttctctt atatectgcc ccaccttctt
 300
 ctggtagcac acagcaacct tgcatagtat ctggtatcat taccttccca atcaacaggc
 360
 cttgatttct tataggactt tttctctcag atttacattg cttctttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggccggggt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
 180
 ttcgacgcag cggctgaact ctctcgcgaa ttgttgaaca ccacgagcct gggtgaagag
 240
 gacatcgccc gtcagatcga cgcggcgcca gcctccctgg cccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtgggggtc acggtcgtcc
 360
 ctgcccacga tcggtaccct ctctcgggtg gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctggggccg cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
 480
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gccagggcga tgacgggtgaa ggtgcccaacc
 60
 gatccccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cgggtggcaag
 240
 gaacggggccc gcaactacga tgcgggtggcc cagctcgtcg cgcagcgagt cgcgcgggtca
 300
 cacggccgga tcaactgcca acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
           20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
           35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
           50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
           85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgect tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcagggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

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Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
           20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
           35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
           50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
           85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100
Thr Thr Pro Met His Gly
115

105

110

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct cgcaccgcgc cgggtgtgaag cacgggcatg cgggtgtgca agtggcacca
60
cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
120
ccgtctatct ctgtgcccac agctcccccg cttccatgtg acccagaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
240
acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcac cacttgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1 5 10 15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20 25 30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35 40 45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50 55 60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65 70 75 80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85 90 95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Gln Ala
100 105 110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgta
60
gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca
120
ccgacctgca agcgctgatg gccagactcg aattgcta atgacgggtc gagcaactta
180
agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
240
tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
300
ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
360
ttcgatcatc tgccccagg aagaacgcag cacctggtga gtgctgcccg ctacctggaa
420
ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcatcgccgt
480
gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
540
ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
588

<210> 340

<211> 123

<212> PRT

<213> Homo sapiens

<400> 340

Met	Glu	Asp	Thr	Asp	Leu	Gln	Ala	Leu	Met	Ala	Arg	Leu	Glu	Leu	Leu
1				5					10					15	
Ile	Asp	Arg	Val	Glu	Gln	Leu	Lys	Ser	Gln	Asn	Gly	Leu	Leu	Leu	Ala
			20					25					30		
Gln	Glu	Lys	Thr	Trp	Ala	Arg	Xaa	Arg	Ala	His	Leu	Ile	Glu	Lys	Asn
		35				40					45				
Glu	Ile	Ala	Arg	Arg	Lys	Val	Glu	Ser	Met	Ile	Ser	Arg	Leu	Lys	Ala
	50				55					60					
Leu	Glu	Gln	Asp	Tyr	Glu	Leu	Ser	Asn	Ser	Val	Thr	Cys	Arg	Ser	Ser
65				70					75					80	
Thr	Lys	Asn	Ile	Arg	Ser	Ser	Ala	Pro	Arg	Lys	Asn	Ala	Ala	Pro	Gly
			85					90					95		
Glu	Cys	Cys	Pro	Leu	Pro	Gly	Arg	Pro	Lys	Gly	Val	Lys	Ser	Ala	Ala
			100					105					110		
Ala	Ala	Lys	Ser	Ser	Val	Pro	Thr	Ala	Ser	Pro					
			115					120							

<210> 341

<211> 401

<212> DNA

<213> Homo sapiens

<400> 341

ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt
60
gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggtttcttg
120

ctgaacattc ttaaccccaa gctgacaatt ttcttcctgg ccttcctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgcag atgctggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggttg acctggcggt tgcgcagcgc tgaggacgcg t
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5				10						15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
		20					25					30			
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
	35					40					45				
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50				55					60					
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65				70				75						80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85				90						95		
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
		100					105					110			
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
	115						120					125			
Gln	Arg														
	130														

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac
 60
 ggggtgctcca acttcagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
 120
 gcggcgcttc cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttccctacca acgacaacc caccgtgatc gtcaagctcc aacagctttc cnnngggcccc
 240
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgtcttct tcgtgctcca gaacttcctg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catgggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaagggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctctgatgg tgcttacggt
240
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgctg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
      65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

```

<210> 347
 <211> 565
 <212> DNA
 <213> Homo sapiens

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<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgctc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggtctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctacccg agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

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<210> 348
 <211> 188
 <212> PRT
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```

50	55	60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly		
65	70	75
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile		80
	85	90
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu		95
	100	105
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu		110
	115	120
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln		125
	130	135
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu		140
145	150	155
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala		160
	165	170
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala		175
	180	185

<210> 349

<211> 339

<212> DNA

<213> Homo sapiens

<400> 349

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ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggt cggctaccgc tcatacgttt gcggaacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattggt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

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<210> 350

<211> 113

<212> PRT

<213> Homo sapiens

<400> 350

Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala		
1	5	10
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp		15
	20	25
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser		30
	35	40
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg		45
	50	55
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His		60
65	70	75
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His		80

	85		90		95										
Ala	Leu	Ala	Gly	Phe	Arg	Glu	Pro	Gln	Arg	Thr	Leu	Glu	Leu	Phe	Asp
	100						105						110		
Ala															

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgccccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg
 120
 ccgcgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
 180
 agccccctg gggaggcggc accagggagc ctgggccccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccn ntcctcctcc tcctccttgg aggcgctctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
120
gaaccattt cagctgttgt cagcccacac ggctcatgc tgttgctggt gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacggtg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggccc gctactgtgg tcttgtgaac
420
gacacgagcc cttcgagata cgttgtcgtc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattgggtg cgcgggtccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcgccc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgca
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgtc
720
ggttttcttg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg
900
cgcgtgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgggccc
1020
gtcatgtggc ccgatctcga cgccatgctc atgggtgccg tgagcgctca cgtctctttt
1080
gctcgaccgc tggatcatgag cccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcaccg tcgtccgcca tcccagaccg ctgcgcattg ctggtctggc cgcgcagccc
1260
ttcacatcgc gtctggtcaa gaagtttgag ctcccggcca gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcacgatga gacggctctc gaaccctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgccggaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

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Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
 20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
 100          105          110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
 115          120          125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
 130          135          140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
 145          150          155          160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
 165          170          175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
 180          185          190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
 195          200          205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
 210          215          220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
 225          230          235          240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
 245          250          255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
 260          265          270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
 275          280          285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
 290          295          300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
 305          310          315

```

<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

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nggatccac ctcctggaat ggaaaccac ataccagttc tcttcctcga tttgaatgcg
 60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
 120

```

ctgccaagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttcctgtggt
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356

<211> 186

<212> PRT

<213> Homo sapiens

<400> 356

Xaa	Ile	Pro	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1				5					10					15	
Asp	Leu	Asn	Ala	Asp	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly	Pro
			20					25					30		
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Ser	Gln
			35				40					45			
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser	Ala
	50					55				60					
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn	Gly
65					70				75					80	
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr	Val
			85					90						95	
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg	Ile
			100					105					110		
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys	Arg
		115				120					125				
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr	Glu
	130					135					140				
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg	Glu
145				150					155					160	
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser	Asp
			165					170						175	
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg						
			180					185							

<210> 357

<211> 323

<212> DNA

<213> Homo sapiens

<400> 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
 120
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg agggcacgtg aagggttga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcaccatgg gtcagcgagg atn
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70				75					80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
				100											

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcgggctgc aatcgagcag
 60
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
 180
 aagctgaagt tcttcggcga gtacaccgtg ttcgacaacc tggcccacaa ctcggttggt
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

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Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

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gctttgacagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catcccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtgggtc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttggt tccgtgggtt atgaatatga atcctgcccc
300
gatctaatacc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaaggga atggngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

65					70					75					80	
Lys	Val	Phe	Gly	Leu	Ser	Glu	Ala	Phe	Val	Ser	Val	Gly	Tyr	Glu	Tyr	
				85					90					95		
Glu	Ser	Cys	Pro	Asp	Leu	Ile	Leu	Trp	Glu	Lys	Arg	Thr	Thr	Val	Leu	
				100					105					110		
Gln	Gly	Tyr	Glu	Ile	Asp	Ala	Ser	Lys	Leu	Gly	Gly	Trp	Ser	Leu	Asp	
				115					120					125		
Lys	His	His	Ala	Leu	Asn	Ile	Gln	Ser	Gly	Ile	Leu	His	Lys	Gly	Asn	
				130					135					140		
Gly	Glu	Asn	Gln	Phe	Val	Ser										
				145					150							

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<210> 363
<211> 502
<212> DNA
<213> Homo sapiens
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<400> 363
ggtaccaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctgggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaaag
120
cgggtgatgcc tgaccgggtgc tcagggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg ttgacactga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc ctttccccta
300
gggggctctg ggcgccatgg ctttctctgat ctgaccacgc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgaggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

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<210> 364
<211> 136
<212> PRT
<213> Homo sapiens
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<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
 1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

				85					90					95					
Ala	Phe	Met	Lys	Val	Leu	Asn	Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr				
			100					105					110						
Ser	Leu	Cys	Glu	Arg	Ile	Trp	Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu				
		115					120					125							
Tyr	Cys	Gly	Lys	Leu	Phe	Trp	Tyr												
	130						135												

<210> 365
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 365
 atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
 60
 ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctgggtgcc
 120
 cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
 180
 gccaagaagt acattgaggc tggagtttca gagcatgcca ggacccttgg cccaaaaggt
 240
 tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
 300
 tctggccctt ccctcaacat cctcatcaag ctt
 333

<210> 366
 <211> 111
 <212> PRT
 <213> Homo sapiens

Ile	Ser	Thr	Asp	Ala	Ser	Ile	Lys	Glu	Met	Ile	Pro	Pro	Gly	Ala	Leu				
1				5				10					15						
Val	Met	Leu	Thr	Pro	Leu	Ile	Val	Gly	Ile	Leu	Phe	Gly	Val	Glu	Thr				
		20					25					30							
Leu	Ser	Gly	Val	Leu	Ala	Gly	Ala	Leu	Val	Ser	Gly	Val	Gln	Ile	Ala				
		35				40					45								
Ile	Ser	Ala	Ser	Asn	Thr	Gly	Gly	Ala	Trp	Asp	Asn	Ala	Lys	Lys	Tyr				
	50				55			60											
Ile	Glu	Ala	Gly	Val	Ser	Glu	His	Ala	Arg	Thr	Leu	Gly	Pro	Lys	Gly				
65				70				75				80							
Ser	Asp	Pro	His	Lys	Ala	Ala	Val	Ile	Gly	Asp	Thr	Ile	Gly	Asp	Pro				
			85				90				95								
Leu	Lys	Asp	Thr	Ser	Gly	Pro	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Leu					
		100					105					110							

<210> 367
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 367

gcgttcgtcg cactaccg cggcggcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaacc gtgngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgtact caaccacatg accatcgaaa gcttcattcg ccctgaggac
180
cgcgctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
acccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccgaat g
381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1			5					10					15		
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
		20					25						30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35				40						45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50				55					60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65				70					75					80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
				85											

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatac cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
60
acttgcgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtttc cttegccagc tgaacgacct cccacccgaa
240
gagcttcccg acgtcatcga ggacttcttc cgctgtcca ctgatgtcct tctttacat
300
ttccagcaag ctt
313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca caggtggtga cgatcatggat cggcctcatc
 60
 tgcacgcgca ttggcacggg ctttatcaag ccgaacctct ccacgggtggt aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggtttca ttgccgctgc tateggtatg gctctgggtc tgategcctt ctccacgggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

50		55		60											
Phe	Ala	Pro	Ile	Val	Thr	Gly	Leu	Leu	Lys	Asp	His	Tyr	Gly	Tyr	His
65				70					75						80
Val	Gly	Phe	Ile	Ala	Ala	Ala	Ile	Gly	Met	Ala	Leu	Gly	Leu	Ile	Ala
			85						90					95	
Phe	Phe	His	Gly	Arg	Ser	Lys	Leu	Arg	Glu	Leu	Ala	Phe	Asp	Ile	Pro
		100						105					110		
Asn	Pro	Leu	Ala	Pro	Gly	Glu	Gly	Arg	Arg	Met	Val	Leu	Arg		
		115					120					125			

<210> 373

<211> 475

<212> DNA

<213> Homo sapiens

<400> 373

acatgttgga aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
 60
 tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
 120
 gcttctctct ggttctctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
 180
 ttggctgggc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgctg
 240
 catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggacccctac
 300
 accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
 360
 agtgggacca aagcagttct taaagggtcca atccactcag ttcttaaagt aaaaacagtt
 420
 gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcgggtg tgcac
 475

<210> 374

<211> 109

<212> PRT

<213> Homo sapiens

<400> 374

Met	Gly	Met	Trp	Trp	Tyr	Arg	Val	Gly	Cys	Arg	Gly	Pro	Gln	Asn	Trp
1				5					10					15	
Gly	Pro	Pro	Cys	Trp	Lys	Gly	Thr	Val	Gly	Arg	Val	His	Ala	Gly	Ala
			20					25					30		
Leu	Gly	Leu	Thr	Gly	Thr	Trp	Asp	Phe	Phe	Leu	Arg	Gly	Ser	Asp	Gln
		35				40					45				
Pro	Thr	Gly	Val	Glu	Gly	Cys	Gly	Glu	Asn	Val	Trp	Pro	Lys	Asp	Leu
	50				55					60					
Gly	Thr	Arg	Glu	Lys	Gln	Ala	His	Asp	Ala	Pro	Phe	Leu	Gly	Gly	Val
65				70					75					80	
Phe	Ile	Arg	Pro	Val	Ala	Ala	Thr	Val	Ile	Thr	Val	Ala	Glu	Ile	His
			85						90					95	
Thr	Cys	Ser	Thr	Arg	Val	Gly	Gly	Asn	Phe	Ser	Asn	Met			
			100				105								

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcgtt ttttcaccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccgc gcgcactatg
 240
 ggcacggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcggtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
 60
 aggctggaac gagggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cggatgaactt
 300
 gagcgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccgggtcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gttaggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatgttg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatgggtcaa gatgttccaa caatcgtt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

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Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

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nacgcgtcat aggcgggccc agtggaagac cacgccaaca cagttggttg agatccgcgt
60
tgaggggcaag gtcctgcgcg tcccgcgaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcgggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccc tagggttgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcgtgg ccttaagcaa tggtcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggtcg gtggacgacg caaactcgtc
480
atccccacc accttgctta cggtcgcgaa ggaatctccg gtgtgatcgc tggcgggtgag
540
acgctggtct tcgtctgcga ccttgtaaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

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<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

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Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
      50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

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nggagcaaca cctggtcctt gggaaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccggt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgtttagaa cctaggattc tgtttttccc aaacaggatc an
352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

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Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50	55	60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser		
65	70	75
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile		80
85	90	

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 385
 gccggcgcca cgaaatgcaa aatgcgcctt tcaccggacg ccaggttgat cgagccgcca
 60
 gcacctcggg caatgtcttg ggcttgactg gcacacgcaa tcaaagcgag caacaacaca
 120
 caaaaacgca tcatgaggca gacgccaggg aagtgcaga agccgcagca ggccgcgggc
 180
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tcggtggcca
 240
 attcgcggaa cgacagcacc gccagttcca gtcgccgcg cagcaccagg cgacgcaagc
 300
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
 342

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1 5 10 15
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
 20 25 30
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
 35 40 45
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
 50 55 60
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
 65 70 75 80
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
 85 90 95
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
 100 105

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 387
 acgcgtgacg cgccggcatc ggaagcgttg actgcagaga agaccgcgca cgtggctgtg
 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgctgat ctgcccattg cgcggcagca agcgtctgat
 180
 gctgttcgtt ccgagctgct cgaagcgcag caagcatgtg cctcgtgcca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5				10						15	
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
			20					25						30	
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
			35					40						45	
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
			50					55						60	
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65					70					75					80
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
				85						90				95	
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
			100					105						110	
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggctcccccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
 120
 gtattgcgtt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggcgat ccaaggggca acaaagtcct caggaggagg actgggtcaac
 300
 cacgagggtt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcgggtgc tatgagcgtg
60
tcgcacccta tcggtggcat gcacgccttg ttcagegact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcaaac ttttcgcatg cgagtgggcc gatatcgctc ctgacatcat ggtggttggg
420
aaatccatga ctggcggata cctgaccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1 5 10 15
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
 20 25 30
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
 35 40 45
 Asp Val Val Gln Arg Gly Arg
 50 55

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
 60
 gagcgggacc ggtacccggc ttcccggtatt ccgacgggtgt gcatcccggc ttctatcgac
 120
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
 180
 gaggcgatgg acaagattaa ggagtcgggt atcgcgtcca gacgctgctt cgtcgtcgag
 240
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgtgag
 300
 cggatctata ccaacgagga cggatatctcc ctggacgac tagccaacga cgtccattgg
 360
 ttgcggggagt c
 371

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1 5 10 15
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
 20 25 30
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
 35 40 45
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
 50 55 60
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
 65 70 75 80
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
 85 90 95
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
 100 105 110
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
 115 120

<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
 60
 gcgacaggtg gtcttgtagc tggtagaaag gcagtcacaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tggtatctca tactcccat gttgcctggt
 180
 ctccagtttt ttacttgtag ttatttccat tcttctattc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaagt cagcgcagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gcccctaaac atgttgctct tggtaactct tactgggttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacgggtggt
 60
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cggtggggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
 240
 cacgtcgacg gtgaacctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
 300

aagatgggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcn tgcccgccgg ttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag
 480
 gat
 483

<210> 398
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 398
 Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
 1 5 10 15
 Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
 20 25 30
 Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
 35 40 45
 Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
 50 55 60
 Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
 65 70 75 80
 His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
 85 90 95
 Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
 100 105 110
 Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
 115 120 125
 Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
 130 135 140
 Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
 145 150 155 160
 Asp

<210> 399
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 399
 nngggaatga agaccacca gcccttcctt tcctcaaate ttctccaggc ttctgtgcat
 60
 ggctcatcca cccatccact cattcaccca tctatccate cactcatcca cccatccagt
 120
 cattcactca tttgtccate cactcatgta cccatccact cattcgccca tttatccate
 180
 cactcaacca tccactcate caccatcca nctcatcate cgtccagtca cccatctate
 240
 caccatgta tccatccact catccacca tccactcate tgtccatcca cttatccacc
 300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
1 5 10 15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
20 25 30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
35 40 45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
50 55 60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65 70 75 80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
85 90 95
His Leu Ser Thr His Leu Leu Thr
100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtgt
120
caaaatgaaa gatctattga agtttacta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcac ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatggggtc
300
ctctaagttc ttcctggata ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctcccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
660
tgaggattta tagcagctaa agggtaaatt ctgttatgca aaaggtcccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga
780
aaaattcctc ttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggccccagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatcc gccccggaa tgcccacgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagaca
1080
ctgccccggc ctttttccct gcaatcaca ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggtcct ttttccgggt caggattggg tggaccatgc
1200
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg
1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttgggtg
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggt ggaatgagcc agggccagga ccttgccggg aggtttgtgc gggttcttgg
1440
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgcc gactttttgt
1500
cttgaggtg cagggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattg gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ccttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtgat
1800
gcttgagaga gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcattcccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggta gctgctggag aggctggccc cactcacttg ggacaaaagc ttttcttgg
2100
ccagtgggga catcatgcct gggttgcccc tagagtagag caggggcgtg taattaagtc
2160
catgg .
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

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Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1           5           10           15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
          20           25           30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
          35           40           45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
          50           55           60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65           70           75           80
Pro Asn Pro Pro Gly Cys Ala
          85

```

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
cttctgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcgg cgaaattcat
360
gctatgatc
369

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<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1           5           10           15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
          20           25           30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
          35           40           45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
          50           55           60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65           70           75           80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

		85						90					95				
Leu	Ala	Leu	Tyr	His	Leu	Trp	Gln	Ala	Phe	Tyr	His	Arg	Pro	Thr	Leu		
		100						105					110				
Gly	Gly	Ala	Cys	Gly	Glu	Ile	His	Ala	Met	Ile							
		115						120									

<210> 405

<211> 840

<212> DNA

<213> Homo sapiens

<400> 405

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gaattcccgc gcaccagctc gaagctggag cacttttgtt ctatcctgct gaagtgcctc
60
gactcgccct ggaccacgag ggccctgtcg gagacagtgg tggaggagag cgaccccaag
120
ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
180
gtggaggcca ccgtgcccac gctgcagcgg accaagtcac ggatcgagca gggatatcgtg
240
gaccgctcag agacgggagc gctggacaag aaggaggggg agcaagccaa ggcgctgttt
300
gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
360
atgcggcaga ccatcatcaa ggtgatcaag ttcatcctca tcatctgcta caccgtctac
420
tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
480
taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
540
tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
600
cggcgctccc tcaagaagta ctgctttgag tcgatccgtg aggagagcag ctacagcgac
660
atccccgacg tcaagaacga cttcgccctc atgctgcacc tcattgacca atacgaccgg
720
ctctactcca agcgcttcgc cgtcttcctg tcggagggtg gtgagaacaa gctgcggcag
780
ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
840

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<210> 406

<211> 91

<212> PRT

<213> Homo sapiens

<400> 406

Leu	Ile	Cys	Met	Tyr	Thr	Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys		
1				5					10					15			
Lys	Tyr	Ser	Phe	Glu	Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile		
		20						25					30				
Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln		
		35					40					45					
Tyr	Asp	Pro	Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val		

50	55	60
Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu		
65	70	75
Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg		80
85	90	

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 407
 gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgtcccc
 60
 aggtcttact ttgctctgcc tggcttcagg gtgtagggga tggagagctg gacttccagc
 120
 ctgcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
 180
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
 240
 agatgctcgc tcggagtggg tgctctgggt ctgggattcc aaaccaagct gccttctctg
 300
 atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc
 360
 caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct cccacttcct
 420
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt
 480
 gcactgagga ccacagcagc cctcgcatte ccacgggcaa aggggtatgt gtagg
 535

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
 1 5 10 15
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
 20 25 30
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
 35 40 45
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
 50 55 60
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
 65 70 75 80
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
 85 90 95
 Val

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

nggtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttgg
 60
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcgggtg
 360
 acggagcgta cgcgt
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
65				70				75						80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100					105						110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
		115					120					125			

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

ccacatactt caccctcctc acccctcca cctactccac cacctggcag tcgccatcga
 60
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc
 180

tggtcgcagg gcacgtcgta ctggtgag acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tggtgtactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc
 360
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggaggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggg agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccgg cccacatcca gctggacccc ctgtcataca gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttcactc agaggcctac
 240
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgcga cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

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<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

65 70 75 80
Gln Ala Pro Asn Leu Ala Ile Arg Leu Ile Val Ser Asn Pro Pro Glu
 85 90 95
Gly Gln Pro Ile Ser Arg
 100

```
<210> 417
<211> 483
<212> DNA
<213> Homo sapiens
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```
<400> 417
gaattcctcgcg ccgtctctga ggtgggcgag gacacctttg tgcgctccac cgagggagac
60
tacgcggcca acgtcgaggc cgtggtgacc ccagcaccgg cggagaaaga tattgagggc
120
cagccagaag cacaggaaca tgacaccccg ggtacagaga ccattgagaa gctggtcgaa
180
tgggcccagg gcgcaggcat tactgtaaac cccgcggtt tttgttatta taccctcaag
240
tgcattgatga tcaagctcca ccacccggcc gcggagagcg aagagcgcgga gtccgagttg
300
gcggcggttc tcatccctgg cgatcgagag ctggatgaaa agcgccttga ggccgcactc
360
gagccggttg agtttgagtt ggcaggggat aaggactttg cagacaatga cttcctagtc
420
aagggctatg ttggcccgcg cgctttgaac gccaatggca tcaaggtctt ggccgatcca
480
cgc
483
```

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<210> 418
<211> 161
<212> PRT
<213> Homo sapiens
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<400> 418															
Glu	Phe	Leu	Ala	Val	Ser	Glu	Val	Gly	Glu	Asp	Thr	Phe	Val	Arg	Ser
1				5					10					15	
Thr	Glu	Gly	Asp	Tyr	Ala	Ala	Asn	Val	Glu	Ala	Val	Val	Thr	Pro	Ala
			20					25					30		
Pro	Ala	Glu	Lys	Asp	Ile	Glu	Gly	Gln	Pro	Glu	Ala	Gln	Glu	His	Asp
		35					40					45			
Thr	Pro	Gly	Thr	Glu	Thr	Ile	Glu	Lys	Leu	Val	Glu	Trp	Ala	Gln	Gly
	50					55					60				
Ala	Gly	Ile	Thr	Val	Asn	Pro	Arg	Val	Val	Cys	Tyr	Tyr	Thr	Leu	Lys
65					70					75					80
Cys	Met	Met	Ile	Lys	Leu	His	His	Pro	Ala	Ala	Glu	Ser	Glu	Glu	Arg
				85					90					95	
Glu	Ser	Glu	Leu	Ala	Ala	Val	Leu	Ile	Pro	Gly	Asp	Arg	Glu	Leu	Asp
			100					105					110		
Glu	Lys	Arg	Leu	Glu	Ala	Ala	Leu	Glu	Pro	Val	Glu	Phe	Glu	Leu	Ala
	115						120					125			
Gly	Asp	Lys	Asp	Phe	Ala	Asp	Asn	Asp	Phe	Leu	Val	Lys	Gly	Tyr	Val

130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt
 60
 cggatccata agtaccggcc gccagggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtggggtg ggctgagctc
 180
 aagccccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaacttctag taagcgcccc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 tttcagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacgggatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

50		55		60											
Thr	Leu	Ser	His	Thr	Asn	Val	Leu	Ser	Pro	Glu	Asn	Val	Lys	Asp	Phe
65					70					75					80
His	Gln	Pro	Leu	Pro	Asp	Ser	Pro	Asn	Leu	Glu	Asn	Val	Met	Ser	Thr
			85						90					95	
Leu	Gln	Ile	Met	Tyr	Thr	Leu	Phe	Val	Gln						
			100						105						

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 421
 ggatccacca tgatggagcc caccaccca tcctcagtc acctgctgca gcttctccat
 60
 aaccaacac aggtcaatct tgtctcccta aacacacat gtgctctcat gctgccatgg
 120
 ttgacctggg gccctctcta cctcctctgc tttctggaga acccttgac tcctccaag
 180
 ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
 240
 ttcataaga ttggttcact gtcagccct gaccagaacg tgtgttttag gaaagcagga
 300
 accaagtctt accaatgtct gtagtcccag cctccacct ggcatacagt aggtgctcat
 360
 tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
 406

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

Met	Met	Glu	Pro	Thr	His	Pro	Ser	Ser	Val	His	Leu	Leu	Gln	Leu	Leu
1				5					10					15	
His	Asn	Pro	Thr	Gln	Val	Asn	Leu	Val	Ser	Leu	Asn	Thr	Pro	Cys	Ala
			20					25					30		
Leu	Met	Leu	Pro	Trp	Phe	Ala	Trp	Gly	Pro	Leu	Tyr	Leu	Leu	Cys	Phe
	35						40				45				
Leu	Glu	Asn	Pro	Cys	Thr	Pro	Pro	Lys	Pro	Ser	Ser	Trp	Lys	Val	Asn
	50				55					60					
Ser	Gln	His	Met	Ser	Leu	Ala	Gln	Pro	Leu	Leu	Arg	Gly	Phe	Met	Lys
65					70					75				80	
Ile	Gly	Ser	Leu	Ser	Ala	Pro	Asp	Gln	Asn	Val	Cys	Phe	Arg	Lys	Ala
			85					90						95	
Gly	Thr	Lys	Ser	Tyr	Gln	Cys	Leu								
			100												

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423

ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
 60
 gageccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgcttcttg gccctcgcaa atggctccct gttggtgccc
 240
 ctcttgagtg ccaaggaggc gggcgctctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctacgt caatacgctt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aacccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggacccg gcggaggagc agcgctgtgg caacggggac
 600
 ccctctcggt acgtttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	Gly	Gly
1				5				10						15	
Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	Gly	Val
			20					25						30	
Gly	Ala	Glu	Glu	Gly	Glu	Gly	Glu	Gly	Asp	Gly	Asp	Leu	Leu	Thr	Gln
			35					40						45	
Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	Pro	Pro
			50					55						60	
Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	Val	Pro
65					70					75					80
Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	His	Asn
				85						90				95	
Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	Ala	Thr
			100							105				110	
Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	Gly	Gln
			115											125	
Ala	Pro	Thr	Ser	Glu	Arg	Lys	Ser	Thr	Ala	Lys	Gly	Arg	Gly	Asn	Ser
			130											140	
Val	Leu	Pro	Ser	Lys	Pro	Glu	Gly	Lys	Ile	Lys	Gly	Gln	Gly	Leu	Ala
145					150					155					160
Lys	Val	Ser	Ile	Leu	Gly	Glu	Thr	Glu	Thr	Glu	Pro	Glu	Glu	Asp	Thr
				165						170				175	
Ser	Glu	Gly	Glu	Glu	Ala	Glu	Asp	Gln	Ile	Leu	Ala	Asp	Pro	Ala	Glu

180 185 190
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His
 195 200 205
 Ala

<210> 425
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 425
 ccggccgtcg aagactttga ggacgatgta gctcgacgcg cagcggttacg agccctggag
 60
 tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
 120
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgagggttcc caaaggacga
 180
 catatcgcag cgggcacccg gatgctcgtc gcccttgat ctgctcgtgt ccgtctgcag
 240
 gctatggagg aaggcctcga cgagatcggt tcccggtttg ctgacatctt tcgcaataac
 300
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg
 360
 gactttgccg agcagcatcc tgggtgagcag ctcaccgtct ccctcgagaa tcggacgatc
 420
 aaccttcggt gtcgcacgac ctaccggttc catattgatg acgtcacgcg t
 471

<210> 426
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 426
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1 5 10 15
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
 20 25 30
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
 35 40 45
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
 50 55 60
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
 65 70 75 80
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
 85 90 95
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
 100 105 110
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
 115 120 125
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
 130 135 140
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaaggtag gcagtttgat cgcggctact tgtctccgta tttcatcaac
60
aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaagggtg ttgctaaagc atcgcgccca
180
ttgttgatca ttgcggaaga cggtgaaggc gaagcggttg caaccttggt tgtaaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgctg tacattgaca
420
aaagaaagta caacgattgt tgatggtgcg ggtggtgcag ctaatattac tggtcgtggt
480
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu	Ala	Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro
1				5					10					15	
Tyr	Phe	Ile	Asn	Asn	Gln	Glu	Thr	Met	Asn	Ala	Glu	Leu	Glu	Asn	Pro
			20					25					30		
Phe	Ile	Leu	Leu	Val	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu
		35				40						45			
Pro	Ile	Leu	Glu	Gly	Val	Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile
	50					55					60				
Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr
65				70					75					80	
Met	Arg	Gly	Ile	Val	Lys	Val	Ala	Ala	Ala	Lys	Ala	Pro	Gly	Phe	Gly
			85					90				95			
Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Val	Leu	Thr	Gly	Ser
		100					105					110			
Thr	Val	Ile	Ser	Glu	Glu	Ile	Gly	Ile	Lys	Leu	Glu	Glu	Ala	Thr	Ile
	115					120					125				
Glu	Gln	Leu	Gly	Thr	Ala	Lys	Arg	Val	Thr	Leu	Thr	Lys	Glu	Ser	Thr
	130					135					140				
Thr	Ile	Val	Asp	Gly	Ala	Gly	Val	Ala	Ala	Asn	Ile	Thr	Gly	Arg	Val

145 150 155 160
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
 Glu Lys Leu Gln Glu Arg
 180

<210> 429
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 429
 gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc
 60
 ccgttgcagc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
 120
 ctgggagcgtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
 180
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
 240
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
 300
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcgggtcc
 360
 cagttcagag cctgaagtcc agactctgcc atatcttctt cactacattc caggagtgga
 420
 tcctg
 425

<210> 430
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
 1 5 10 15
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
 20 25 30
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
 35 40 45
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
 50 55 60
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
 65 70 75 80
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
 85 90 95
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
 100 105 110
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
 115 120 125
 Asp Pro
 130

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccggt gcccggaactg cgagcggcgc ttctcctcct cctctcgctt ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
 60
 ctcattggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagtg cctcgcacag ctgtacatgg ccgcacatca gcccggaag
 420
 gctctgacat actacatgcy cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
 600
 tcgattccca tccagcgcgc catggcgcag ctcga
 635

<210> 434

<211> 211

<212> PRT

<213> Homo sapiens

<400> 434

Xaa	Pro	Ala	Ala	Ala	Leu	Gly	Tyr	Asp	Val	Ala	Ala	Ile	Gly	Arg	Glu
1				5					10					15	
Tyr	Leu	Trp	Tyr	Leu	Met	Glu	Glu	Arg	Gly	Ala	Tyr	Ala	Glu	Ala	Ala
			20					25					30		
Ala	Leu	Met	Pro	Leu	Leu	Leu	Arg	Thr	Asp	Arg	Gly	Ala	Trp	Asp	Thr
		35					40					45			
Phe	Val	Cys	Cys	Tyr	Leu	Glu	Arg	His	Gln	Arg	Asp	Ala	Ile	Leu	Pro
	50					55				60					
His	Ile	Pro	Thr	Gln	Asp	Pro	Gln	Leu	Ser	Glu	Met	Val	Tyr	Asp	Leu
65				70					75					80	
Val	Leu	Val	His	Leu	Leu	Gln	His	Asp	Pro	Thr	Gln	Leu	Leu	Ala	Thr
			85					90						95	
Leu	Arg	Ala	Trp	Pro	Ser	His	Ile	Tyr	Ser	Lys	Gln	Ala	Val	Ala	Ala
		100						105					110		
Ala	Ile	Gly	Asp	His	Ala	Arg	Thr	Ser	Arg	Thr	Leu	Leu	Glu	Cys	Leu
		115					120					125			
Ala	Gln	Leu	Tyr	Met	Ala	Ala	His	Gln	Pro	Gly	Lys	Ala	Leu	Thr	Tyr
	130						135				140				
Tyr	Met	Arg	Leu	Arg	Asp	Pro	Cys	Val	Phe	Asp	Leu	Ile	Arg	Glu	Tyr
145				150					155					160	
Asp	Leu	Leu	Ile	Asp	Val	Gln	His	His	Ile	Gly	Thr	Leu	Val	Glu	Leu
			165					170						175	
Asp	Gln	Glu	Cys	Ala	Gly	Ser	Thr	Glu	Pro	Arg	Ser	Ser	Ala	Leu	Met
		180						185					190		
Pro	Leu	Leu	Val	Pro	Tyr	Thr	His	Ser	Ile	Pro	Ile	Gln	Arg	Ala	Met
	195						200						205		
Ala	Gln	Leu													
	210														

<210> 435

<211> 493

<212> DNA

<213> Homo sapiens

<400> 435

nncgtacgtt cgcgtatttt ccgcgcccgga gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggtaacttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatggtga atcgttcgac agcgagctgt tgagttctct gtcgcaagat
 180
 cgaacgcttc aacaaagctg gcagggtat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggagagcc agattacgca aatcggtatg
 420
 gcggcctgcg tgcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
 480
 ccatcgaacg cgt
 493

<210> 436
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp
 1 5 10 15
 Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser
 20 25 30
 Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45
 Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu
 50 55 60
 Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro
 65 70 75 80
 Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro
 85 90 95
 Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu
 100 105 110
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser
 115 120 125
 Asn Ala
 130

<210> 437
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 437
 ntggtaaccg gtgtccctga tatggaccct gctgtgtag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
 120
 attaatacat tctcatacaa aacaatcggt tataaaggct agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagatgt acaaaatcca agtatggtaa cggcattagc gcttggtcat
 240
 tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt ttccactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
 60
 cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcaggggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg
 180
 ctcagcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gccagtact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagccc
 60
 ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
 120
 gacggttgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
 180
 ggcggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggc ccggatgggc
 300
 caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

35	40	45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys		
50	55	60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala		
65	70	75
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala		
85	90	95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile		
100	105	110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala		
115	120	

<210> 443

<211> 430

<212> DNA

<213> Homo sapiens

<400> 443

accggttacg gtcagtgca acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc cttcgccaag atcctctcga cgacctgtc catcggtatcg
120
ggcgggtccgg cggcgtcttc cggccctggc atgggtcatcg gcggagccac tggcgcggca
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag tttcgtcatt
240
gtcggcatga tcgcctgctt cgggtgcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

<210> 444

<211> 143

<212> PRT

<213> Homo sapiens

<400> 444

Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val		
1	5	10
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu		
20	25	30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly		
35	40	45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu		
50	55	60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile		
65	70	75
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly		
85	90	95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala		

	100		105		110										
Pro	Gly	Met	Ile	Ala	Val	Ala	Val	Ala	Gly	Arg	Val	Val	Gly	Asp	Thr
	115		120		125										
Ser	Ile	Tyr	Thr	Ser	Gln	Leu	Lys	Asp	Arg	Leu	Glu	Gly	Asp	Ala	
	130		135		140										

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 445
 ccattggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
 60
 tcttgcttta ttgctcacc tgtccagggt tccctctggt tgtgaggag ctgctgccac
 120
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acttttcctt
 180
 agttttcttt gctcttctgc tctgagtcga gccctggctg gacctttgat cccttctctc
 240
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
 300
 caagtgggaa caagccatga aggagctgca ccccgaaag tctgagggtg ggacacgcgt
 360

<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 446
 Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1 5 10 15
 Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
 20 25 30
 Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
 35 40 45
 Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
 50 55 60
 Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
 65 70 75 80
 Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
 85 90 95
 Gly Leu Pro Arg Gly
 100

<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 447
 acgcgtgaag ggggaaattg ctggtgccac ctgaggatta atcattaccc tggaaccctt
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaaggggaat ggggggcccc catggccagc tggacctgat
 180
 cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agcccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgagaggca accttcccca gtgccccaac
 300
 catagcggtt tcccccaaac accctcagga aggagggacc actacctgtg cagggggggc
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccctctcacc cccattgcct
 420
 ttctctccta ctccacctg gccagcttcc ctgagtgcc ctcctgcctc agtgcccctt
 480
 cacgcgt
 487

<210> 448

<211> 117

<212> PRT

<213> Homo sapiens

<400> 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20					25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35					40					45			
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65				70					75					80	
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85					90					95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100				105						110		
Cys	Pro	Phe	Thr	Arg											
			115												

<210> 449

<211> 353

<212> DNA

<213> Homo sapiens

<400> 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
300
gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
353

<210> 450
<211> 117
<212> PRT
<213> Homo sapiens

<400> 450
Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
1 5 10 15
Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
20 25 30
Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
35 40 45
Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
50 55 60
Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
65 70 75 80
Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
85 90 95
Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
100 105 110
Arg Arg Arg Gln Arg
115

<210> 451
<211> 444
<212> DNA
<213> Homo sapiens

<400> 451
gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
60
gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgtaaatggt
120
gcagaagttt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt
180
ttgggagaga ctttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
240
gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactt ttcagcctcc
300
aatgctgcag tggctgaact taaaccggat tgttgattg atgatgtcat acatcatgaa
360
gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
420
gaaaaaatgt atttcagaaa attt
444

<210> 452
<211> 148
<212> PRT

<213> Homo sapiens

<400> 452

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Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

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gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gcccagatg acctggggct
120
tgaaaggcac tcccgctggg tgcttcctgg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggtctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttctctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

20						25					30				
Gln	Ala	Ser	Pro	Ser	Gln	Asn	Ala	Pro	Val	Gly	Leu	Arg	Ala	Gln	His
35						40						45			
Leu	Pro	Trp	Ser	Trp	Gly	Cys	Ser	Ala	Gln	Thr	Gly	Pro	Ala	Ala	Pro
50						55				60					
Leu	Pro	Pro	Thr	Cys	Ser	Gln	Glu	Ala	Pro	Ser	Gly	Ser	Ala	Phe	Gln
65				70						75				80	
Ala	Pro	Gly	His	Leu	Gly	Pro	Phe	Leu	Asp	Asn	Arg	Gly	Asp	Cys	Ile
85								90				95			
Phe	Gln	Leu	Tyr	Asn	Pro	Ser	Pro	His	Trp	Pro	Pro				
100					105										

<210> 455

<211> 602

<212> DNA

<213> Homo sapiens

<400> 455

cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
accatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccacccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct tttctctctcg cccctctca ctgacctggt tttgatgcc
360
gacagcacag atgggctagg gaggcagggtg gggaagcaga gatctgcgtc tcttggagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggtcacgc
600
gt
602

<210> 456

<211> 100

<212> PRT

<213> Homo sapiens

<400> 456

Met	Pro	Thr	Leu	Pro	Pro	Leu	Thr	Leu	Thr	Leu	His	Phe	Pro	Leu	Ser
1				5					10					15	
Thr	His	His	His	Arg	Cys	Tyr	Cys	Met	Cys	Leu	Leu	Thr	Leu	Thr	Ala
			20					25					30		
His	His	Pro	His	Trp	Asn	Val	Arg	Thr	Thr	Lys	Ala	Gly	Leu	Leu	Ala
		35					40					45			
Ala	Leu	Ala	Thr	Ala	Gly	Ser	Pro	Glu	Leu	Cys	Arg	Val	Leu	Gly	Thr

50 55 60
 Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
 65 70 75 80
 Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
 85 90 95
 Leu Ala Thr Tyr
 100

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 457
 acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
 60
 agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
 120
 tcccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
 180
 ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
 240
 tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcggcgg
 300
 gagcaccggg acgccggggc gccg
 324

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 458
 Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
 1 5 10 15
 Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
 20 25 30
 Ile Val Lys Pro Gly Leu Pro Leu Leu Ala Ala Thr Arg Gln Pro
 35 40 45
 Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
 50 55 60
 Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
 65 70 75 80
 Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
 85 90 95
 Gly Gly Ser Thr Gly Thr Pro Gly Arg
 100 105

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc
60
gggtgtcgaa cacgacactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
120
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtgggt
180
tatgtgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
240
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc
300
ctcctcaaag ccgatcatcg gcatgccagg tttgtgggtg aatgcttcga tcaacacact
360
aggatcggtg gggccacca catacaccga gcggcaatcg agcggatacg acctc
415

<210> 460

<211> 105

<212> PRT

<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
		20						25				30			
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35					40					45			
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50				55				60						
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65				70					75					80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
			85					90					95		
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

<210> 461

<211> 357

<212> DNA

<213> Homo sapiens

<400> 461

acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac
60
cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
120
gctcctagaa ccagctcaga gagtcccggg gtcgggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcattctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtgggtgca tgcgaggaat gcgatcgtat cctgggtgcgt
 120
 accggagagt ccatctgagc ccttcttgtg gcggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgagg cagcgggtgag ttgtcgagga aagtcggggc
 240
 tccatagagc aggggtggtgg gtaacgcca cccgggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgag
 360
 tcatcgggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgcggac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
115          120          125

```

<210> 465

<211> 438

<212> DNA

<213> Homo sapiens

<400> 465

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gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggttat cattacgggtt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattgggt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466

<211> 143

<212> PRT

<213> Homo sapiens

<400> 466

```

Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

65					70					75					80
Glu	Thr	Ala	Leu	Ala	Gly	Val	Thr	Ile	His	Ala	Ala	Lys	Ala	Leu	Gly
				85					90					95	
Ile	Ser	Asp	Ser	His	Gly	Thr	Leu	Glu	Val	Gly	Lys	Val	Ala	Asp	Phe
				100					105					110	
Val	Cys	Trp	Asp	Val	Glu	Ser	Pro	Gly	Glu	Leu	Cys	Tyr	Trp	Leu	Gly
				115					120					125	
Glu	Gln	Leu	Val	Lys	Gln	Arg	Ile	Gln	His	Gly	Val	Ser	His	Glu	
				130					135					140	

```
<210> 467
<211> 460
<212> DNA
<213> Homo sapiens
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```

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgagggaac ttcggagctt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctgggtcc acttttccct ctctaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
360
ttcctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggg tctgtatggt gccgcaattg
460

```

```
<210> 468
<211> 118
<212> PRT
<213> Homo sapiens
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```

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
 1          5          10          15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
          20          25          30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
          35          40          45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
          50          55          60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65          70          75          80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
          85          90          95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
          100          105          110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469
<211> 381
<212> DNA
<213> Homo sapiens

<400> 469
cttgtgcaca cgttattttt ccaatacaaa tagtttaaaa agtaaactcc aaatacctat
60
aagccccctc aaagcacctt ccaaataatga accttggttaa tgcccaaggt ccagaggggt
120
ccccagaaa ggcccaggag cctggggcat gggaaagctg tcggggctcc catgctgact
180
ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
240
tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
300
ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga
360
agtccatcgg caaagaaaga c
381

<210> 470
<211> 110
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
1 5 10 15
Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
20 25 30
Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
35 40 45
Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
50 55 60
Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
65 70 75 80
Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
85 90 95
Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
100 105 110

<210> 471
<211> 378
<212> DNA
<213> Homo sapiens

<400> 471
accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcca
60
gaggtcttcc tgggttaactg gtcccgccgc ggcgacgatg gccgcttcct gtggccgngg
120

cttggcgaaa acttcccggg cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgccgtg acccgaagga atgggaaggc
 300
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
		20						25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
		35					40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
	50					55				60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65				70					75					80	
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
			85						90					95	
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
		100						105					110		
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
		115					120					125			

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc
 180
 ctgcttccat ttccctctcc aggggaacagg tgtacctccc ctctccctg tcctctcag
 240
 atgccccagg ggctctctac ttcatctctg ccgacctgc caggagtggc ctcaggggta
 300
 gaggctccta gttggagaat ttgcttgacg gaaggtgaa
 339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
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 agcgcttggc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacacagc cataatcccc
 180
 aatgctggga ctcttcagta aaggaagaga tggttttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttgtaga agtgggttgt tcattctggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

65					70					75					80
Pro	Ala	Trp	Arg	Arg	Gly	Leu	Ser	Gly	Arg	Arg	Trp	Gly	Ala	Pro	Ser
				85					90					95	
Lys	Ala	Trp	Lys	Glu	Ala	Gln	Ser	Leu	Glu	Gly	Thr	Leu	His	Ala	
			100					105					110		

<210> 477

<211> 422

<212> DNA

<213> Homo sapiens

<400> 477

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gactctcccg aggtggaacg ggcaactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgcccac gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgccttc gatgccggtc
300
ttcgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtccctt ccccgattc
360
cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

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<210> 478

<211> 140

<212> PRT

<213> Homo sapiens

<400> 478

Thr	Arg	Gly	Arg	Ala	Ser	Val	Leu	Lys	Glu	Met	Val	Asn	Gly	Thr	Leu
1				5					10					15	
Ile	Asn	Gly	Trp	Asp	Ser	Pro	Glu	Val	Glu	Arg	Ala	Leu	Asp	Leu	Cys
			20					25					30		
Met	Ala	Cys	Lys	Gly	Cys	Ala	Arg	Asp	Cys	Pro	Thr	Gly	Ile	Asp	Met
		35					40					45			
Ala	Ser	Tyr	Arg	Ser	Thr	Val	Leu	Asp	Glu	Lys	Tyr	Arg	His	Arg	Leu
	50					55					60				
Arg	Pro	Arg	Ser	His	Leu	Thr	Met	Gly	Leu	Leu	Pro	Met	Trp	Glu	Arg
65				70						75				80	
Leu	Leu	Asn	Arg	Thr	Pro	Gly	Ala	Pro	Ser	Leu	Ala	Asn	Ala	Val	Leu
				85					90					95	
Ser	Met	Pro	Val	Phe	Ala	Arg	Leu	Ala	Arg	Trp	Thr	Ala	Gly	Val	Asp
			100					105					110		
Gln	Arg	Arg	Pro	Leu	Pro	Arg	Phe	Gln	Pro	Ser	Ala	Arg	Leu	Ala	Ser
		115					120					125			
Pro	Gln	Ala	Ala	Pro	Val	Lys	Glu	Ile	Val	Ala	Asp				
	130					135					140				

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
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 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac
 180
 gccacccggg tggcgggtgat gagcgagggc aggggtgggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgagca cccctacacc cgcaagctgc tggccgccgc cagccccttg
 300
 gagaaacttg aaaacgggtg ctaccgcac cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
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 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc
 120
 cctgccctgc cggcttgccg tggcttcttc agtggttagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgccctgtct cccagcaggg cccacaancca
 240
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag
 360
 taaatcccca gtcatttgag tttccctca gcgccagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgct t
 441

<210> 482
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 482
 Lys Leu Leu Thr Val Ala Phe Ser Leu Leu Asn Met Ser Ser Ile Ser
 1 5 10 15
 Pro Thr Tyr Trp Ala Lys Ser Cys Leu Cys Phe Gly Thr Ser Ser Lys
 20 25 30
 Thr Thr Pro Leu Asp Gly Ala Phe Pro Ala Leu Pro Ala Cys Ala Gly
 35 40 45
 Phe Leu Ser Val Arg Ile Thr Ile Thr Leu His His Glu Ser Arg Arg
 50 55 60
 Pro Ser Pro Cys Asp Cys Cys Pro Cys Ser Gln Gln Gly Pro Gln Xaa
 65 70 75 80
 Pro Ser Pro Gly Pro Gly Ser Arg Trp Val Ala Asp Ala Gln Glu Trp
 85 90 95
 Gly Ser Gly Ser Ala Ser Ser Pro Ala Gly Pro Gly Asn Arg Cys Pro
 100 105 110
 Val Pro Ala Pro Gly Asn Pro Gln
 115 120

<210> 483
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 483
 acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggg
 60
 caagggttgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttta aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggccc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
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 gccagtttcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
 120
 cgggggatac caaaggaatc ttgtcgaggg cttecgggcc ctcgacgtgg atcacctgta
 180
 cccgacggac gtggggaagc cgtcccgcga gctcacggga ctccgcgaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgatc gcctcagcgg
 300
 tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
 360
 cattcccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

65		70		75		80									
Pro	Arg	Ser	Pro	Gln	Arg	Trp	Phe	Pro	Thr	Ser	Ala	Gly	Thr	Trp	Arg
			85					90						95	
Arg	Val	Ala	Trp	Arg	Ser	Pro	Leu	Cys	Arg	His	Ser	His	Ser	Ser	
			100					105					110		

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 487
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 cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggtaagaat
 120
 agtgagtttc gtgtggctgt gacgccggcg ggtgttcattg cgttggttg tctgggtcat
 180
 gaggtgttg ttcaggctgg tgctggtgtg gggtcgggta ttccggattc ggattttgtg
 240
 ggtgctggtg cgcgggttgt gggatgatgt gagtcggtgt ggggtgatgc tgatttggtg
 300
 ttgaaggatga aggagcctgt tgcggaggag tatgggcggt tgcattgaggg tttggttctt
 360
 ttacgtatc ttcatttggtc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
 420
 gtgacgtcga ttgcgtatga gacggtggag ttggccgat
 459

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 488
 Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
 1 5 10 15
 Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
 20 25 30
 Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
 35 40 45
 Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
 50 55 60
 Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
 65 70 75 80
 Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
 85 90 95
 Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
 100 105 110
 Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
 115 120

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
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 aaccagcacg gttgctacaa agtgcgcttt ccatttaccc gcgatcaaaa gccagcact
 120
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgcgt accaaactcg gaaaccccga gcatggtcgt tgagcgtaac
 300
 gccacccaga gcggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct gggcgccct ggcggcaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccggcggc
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly
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Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe
			20					25					30		
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg
		35					40					45			
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu
	50					55					60				
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg
65					70					75				80	
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val
			85					90					95		
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His
			100					105					110		
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly
		115					120					125			
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala
	130					135					140				
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe
145					150					155				160	
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg
			165					170						175	
Gly	Pro	Gly	Gly												

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
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 gcatcgggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcgggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg
 240
 tcgacgtgtc ggtcggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcctc ggcattccat
 480
 tcctcccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgag cgcattgaca gtacgaagcc aacgttgctg catcacaggg
 600
 ttcattggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgcccgcgac atcctcggcg tcattggtcga catggaattg cgcgtcagct
 720
 gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

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 cctcgcggcg atcggatgtg ttctgagaa tatagctccc ttcgatcccg accaggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgacca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatggttgat cccgggtctgc agcaggcctt cggcgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag
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 atcaatgcca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
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 720
 ggcctttttt cggcccgga gtcgcgggta attgttgatg gcgagcaaata agacatgggt
 780
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 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met	Thr	Leu	Ala	Leu	Asp	Ile	Pro	Leu	Asn	Asp	Ser	Gln	Phe	Ser	Ala
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Gln	Arg	Lys	Ser	Glu	Val	Leu	Val	Glu	Ala	Leu	Pro	Trp	Ile	Arg	Arg
			20					25					30		
Phe	Gln	Gly	Arg	Thr	Val	Val	Val	Lys	Tyr	Gly	Gly	Asn	Ala	Met	Val
		35				40						45			
Asp	Pro	Gly	Leu	Gln	Gln	Ala	Phe	Ala	Asp	Asp	Ile	Val	Phe	Met	Ala
	50				55						60				
Ser	Val	Gly	Ile	Arg	Pro	Ile	Val	Val	His	Gly	Gly	Gly	Pro	Gln	Ile
65					70				75					80	
Asn	Ala	Met	Leu	Ala	Glu	Ser	Ala	Thr	Pro	Val	Glu	Phe	Arg	Asn	Gly
			85					90						95	
Leu	Arg	Val	Thr	Ser	Pro	Glu	Val	Met	Glu	Val	Val	Arg	Met	Val	Leu

	100		105		110										
Val	Gly	Gln	Val	Gly	Arg	Gln	Leu	Val	Asn	Arg	Ile	Asn	Ala	Tyr	Ala
	115		120		125										
Pro	Leu	Ala	Ala	Gly	Met	Ser	Gly	Glu	Asp	Phe	Gly	Leu	Phe	Ser	Ala
	130		135		140										
Arg	Lys	Ser	Arg	Val	Ile	Val	Asp	Gly	Glu	Gln	Ile	Asp	Met	Gly	Leu
145			150		155									160	
Val	Gly	Asp	Ile	Val	Asp	Val	Asn	Ile	Asp	Leu	Val	Ile	Ser	Met	Leu
	165		170		175										
Asp	Arg	Gly	Gln	Ile	Pro	Val	Ile	Ala	Pro						
	180		185												

<210> 495

<211> 514

<212> DNA

<213> Homo sapiens

<400> 495

gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
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120
cggtggccga tccaccggga tccccggcc ttcgatgacc ttgagcccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcgggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggccaactg ctgtgggacc ttgg
514

<210> 496

<211> 171

<212> PRT

<213> Homo sapiens

<400> 496

Ala	Arg	Asp	Thr	Gly	Ala	Pro	Ile	Ser	Val	Pro	Val	Gly	Asp	Val	Thr
1				5					10				15		
Lys	Gly	His	Val	Trp	Asn	Val	Thr	Gly	Asp	Val	Leu	Asn	Ala	Xaa	Ser
			20					25					30		
Leu	His	Asn	Arg	Gly	Asp	Xaa	Glu	Arg	Trp	Pro	Ile	His	Arg	Asp	Pro
	35					40					45				
Pro	Ala	Phe	Asp	Asp	Leu	Glu	Pro	Glu	Thr	Glu	Met	Leu	Glu	Thr	Gly
	50				55					60					
Ile	Lys	Val	Leu	Asp	Leu	Leu	Thr	Pro	Tyr	Val	Lys	Gly	Gly	Lys	Ile
65				70				75						80	
Gly	Leu	Phe	Gly	Gly	Ala	Gly	Val	Gly	Lys	Thr	Val	Leu	Ile	Gln	Glu

				85					90					95					
Met	Ile	Tyr	Arg	Ile	Ala	His	Asn	Phe	Gly	Gly	Thr	Ser	Val	Phe	Ala				
				100					105					110					
Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Leu	Ile	Asn	Glu	Met				
		115						120					125						
Asp	Glu	Ala	Gly	Val	Leu	Lys	Asp	Thr	Ala	Leu	Val	Phe	Gly	Gln	Met				
		130					135					140							
Asp	Glu	Pro	Pro	Gly	Thr	Arg	Tyr	Glu	Leu	Ser	Arg	Trp	Gln	Pro	Cys				
145					150					155					160				
Gly	Pro	Cys	Leu	Val	Asn	Cys	Cys	Gly	Thr	Leu									
				165					170										

<210> 497

<211> 662

<212> DNA

<213> Homo sapiens

<400> 497

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acgcgtcctg ggatctcaac cccagcagtc tggcttggtt ctcattccca caatttcctg
60
ggttccacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgctcagc acaggcctgg gacctcccc ggcaggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gacccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

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<210> 498

<211> 191

<212> PRT

<213> Homo sapiens

<400> 498

Met	Asn	Glu	Glu	Lys	Thr	Gln	Pro	His	Lys	Arg	Asp	Thr	Arg	Trp	Arg				
1				5					10					15					
Gly	Glu	Thr	Gln	Gln	Ser	Ser	Phe	Leu	Ser	Val	Asp	Ser	Glu	Gln	Arg				
		20					25						30						
Arg	Gly	Ala	Pro	Ser	Phe	Val	Phe	Ser	Ser	Ser	Gly	Glu	Arg	Met	Asp				

```

      35      40      45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
  50      55      60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
65      70      75      80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85      90      95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100      105      110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115      120      125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130      135      140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
145      150      155      160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165      170      175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180      185      190

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<210> 499

<211> 444

<212> DNA

<213> Homo sapiens

<400> 499

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acgcgtgaag ggtgggcagt gttgagctga gtagagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttccta agcagtctat acgtgagaag ccctttcttc
120
aagtgaaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcctcaactg gggggttgga ggagggtact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tcctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

```

<210> 500

<211> 105

<212> PRT

<213> Homo sapiens

<400> 500

```

Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1      5      10      15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20      25      30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35          40          45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
      50          55          60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
65          70          75          80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85          90          95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100          105

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<210> 501
 <211> 800
 <212> DNA
 <213> Homo sapiens

<400> 501
 agatctgac cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
 60
 ggtactcctt attcaatgag aggcctgagg tgagaccgc catgcggcgc gtggatcgca
 120
 tgggtgtagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
 180
 gaccttgtagc tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
 240
 gaagtttatt ctcccatgga tgatgctggc ttcccggtca aagctgagga gtttgtggtg
 300
 ctttctcagg aaccttctgt cacggaaacc attgcacca aaattgcaag acctttcata
 360
 gaggcctca agagtattga gtatctggag gaggatgcc agaagtccgc acaggagggg
 420
 gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
 480
 gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
 540
 tatgctttta attacctgga atcttgaggc agggcctgag agagcacgct ggcgcgtact
 600
 tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
 660
 tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
 720
 cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agcttttagct
 780
 atcttgcttc agaaactgaa
 800

<210> 502
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 502
 Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
 1 5 10 15
 Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503

<211> 538

<212> DNA

<213> Homo sapiens

<400> 503

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nnacgcgttg tcgtctctcc gatcattgat tttgttgtat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgcagct attggaaggg gaagggtccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggcccct tcacgcgt
538

```

<210> 504

<211> 179

<212> PRT

<213> Homo sapiens

<400> 504

```

Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

				85					90					95					
Lys	Asn	Ala	Pro	Leu	Leu	Leu	Pro	Asp	Val	Ile	Lys	Val	Ser	Thr	Arg				
			100					105					110						
Ser	Ser	Glu	His	Phe	Phe	Ser	Val	Phe	Leu	Asn	Ile	Asn	Glu	Thr	Phe				
		115					120					125							
Lys	Leu	Met	Glu	Gln	Leu	Ala	Asn	Ile	Ala	Met	Arg	Gln	Leu	Leu	Asp				
	130					135					140								
Asn	Glu	Gly	Phe	Glu	Gln	Asp	Arg	Ser	Leu	Pro	Lys	Leu	Lys	Arg	Lys				
145					150				155						160				
Ser	Pro	Lys	Lys	Val	Ser	Ala	Leu	Lys	Arg	Asp	Leu	Asp	Ala	Trp	Ala				
				165				170						175					
Leu	His	Ala																	

<210> 505

<211> 381

<212> DNA

<213> Homo sapiens

<400> 505

gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60atgctcgggt acgacngctc aagaacctgt cgcattgacct tgctcaccgg gcagctggac
120gacctctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180gaggtcgatc agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240gtggaaccac gcgccgcctg gcccgaggg atggacgcc tccaggttgc gctcaagggt
300cgcattcagt ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360ggttggggag gggcgctgcg c
381

<210> 506

<211> 127

<212> PRT

<213> Homo sapiens

<400> 506

Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1 5 10 15Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20 25 30Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35 40 45Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50 55 60Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65 70 75 80Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85 90 95

Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

	100		105		110									
Val	Ile	Ala	Arg	Leu	Ser	Asp	Leu	Gly	Trp	Gly	Gly	Ala	Leu	Arg
	115			120								125		

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
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 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaa
 120
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tcctcctccc aaggtggtgc cgttcagtcg gagtcgctcg tcaatcacct gtacacgctc
 240
 gccaccgcca tcccagcagat ctgctgcctc ggcgctgccc tgctcatgct gggctaccg
 300
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcagat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggctcg caagttcagt cccaaagatg tcacgctcta tctaattggac
 60
 ttccgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttgtccga ctacggtggt ggtacactag agctctaccg tcaggctagc
 240
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
 300
 gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc
 360

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
1				5					10				15		
Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20					25					30		
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
			35				40					45			
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
	50					55				60					
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65					70				75					80	
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
				85				90						95	
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
				100				105						110	
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
			115				120								

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

ntcgcaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
 60
 actgcgttcg gcgatgccgg catcggccag atcgggcgca agatgcagga cgatctcgac
 120
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
 180
 ggggcctcct atggcggcta tgccgcgatg tggggcgaga tccgcaatcc cgaacgctat
 240

cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaatt ataaccggcg
 300
 ctatctcgac aaggaggcgg gcaagcgtg gccgccccgn tcaaccggcg aaccggaatt
 360
 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
 nnatgcagac tagaagatgg catgacgggt ttggctggcg gtttcgggct atgcggcatt
 60
 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatggtgt cttcttatgt gggtgaaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
 300
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

```

      1           5           10           15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85           90           95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100          105          110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115          120

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<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

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<400> 515
gcgtgggacg agaaggccgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttcctct cggacgacgg gcagatcctg
180
cgggcgttcc agaaggccgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgatc
360
gccgacctga ccggtgcgcc gttgtac
387

```

<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

```

<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
      1           5           10           15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
      20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
      35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
      50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
      65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

[illegible]

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<210> 517
<211> 377
<212> DNA
<213> Homo sapiens
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<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
60
agacccttcc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg
120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctcttgggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agaccctag ctggagaggg cagaaggggt
240
ccctgagctt ccccaggaga agggggggcca atttggagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377
```

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<210> 518
<211> 118
<212> PRT
<213> Homo sapiens
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```

<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
 1           5           10           15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
          20           25           30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
          35           40           45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
 50           55           60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65           70           75           80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
          85           90           95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
          100          105          110
Pro Thr Ser Pro Ser Arg
          115

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<210> 519
<211> 311

<212> DNA

<213> Homo sapiens

<400> 519

gcgcgccagg gggaaggag agaaaacaca gaaaaatgag ggggaaatac cagatactga
 60
 agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatggt agaatatcca
 120
 aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc
 180
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcca aacctggaat
 240
 tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc
 300
 cagaacttaa g
 311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1				5					10					15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
			35				40					45			
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50					55					60				
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65					70				75					80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85						90						

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

nnngatgccca cgccggtcta cggaatctcc accggcttcg gcgcgcttgc ccgcccgcac
 60
 attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgctccca cgcgcccggc
 120
 accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc
 180
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 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
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 Glu Gly Glu Val Arg
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 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
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 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
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 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
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 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
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 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
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 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
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 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
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<211> 290

<212> PRT

<213> Homo sapiens

<400> 526

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Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe	Pro
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Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
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Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu	Leu
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His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala	Ser
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Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
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Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile					
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Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr					
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<211> 5343

<212> DNA

<213> Homo sapiens

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<211> 886

<212> PRT

<213> Homo sapiens

<400> 528

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Leu	Pro	Glu	Asp	Ser	Glu	Thr	Ala	Tyr	Asp	Trp	Glu	Tyr	Ala	Gly	Phe

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Thr	Pro	Cys	Thr	Ala	Thr	Cys	Leu	Gly	Gly	His	Gln	Glu	Ala	Ile	Ala
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Val	Cys	Leu	His	Ile	Gln	Thr	Gln	Gln	Thr	Val	Asn	Asp	Ser	Leu	Cys
				85					90					95	
Asp	Met	Val	His	Arg	Pro	Pro	Ala	Met	Ser	Gln	Ala	Cys	Asn	Thr	Glu
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Pro	Cys	Pro	Pro	Arg	Trp	His	Val	Gly	Ser	Trp	Gly	Pro	Cys	Ser	Ala
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Gly	Glu	Thr	Pro	Ala	Pro	Pro	Glu	Glu	Cys	Arg	Asp	Glu	Lys	Pro	His
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Ala	Leu	Gln	Ala	Cys	Asn	Gln	Phe	Asp	Cys	Pro	Pro	Gly	Trp	His	Ile
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Glu	Glu	Trp	Gln	Gln	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Thr	Gln	Asn
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Arg	Arg	Val	Thr	Cys	Arg	Gln	Leu	Thr	Asp	Gly	Ser	Phe	Leu	Asn	
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Cys	Ala	Arg	Thr	Asp	Cys	Pro	Pro	His	Leu	Ala	Val	Gly	Asp	Trp	Ser
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Lys	Cys	Ser	Val	Ser	Cys	Gly	Val	Gly	Ile	Gln	Arg	Arg	Lys	Gln	Val
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Cys	Gln	Arg	Leu	Ala	Ala	Lys	Gly	Arg	Arg	Ile	Pro	Leu	Ser	Glu	Met
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Met	Cys	Arg	Asp	Leu	Pro	Gly	Leu	Pro	Leu	Val	Arg	Ser	Cys	Gln	Met
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Pro	Glu	Cys	Ser	Lys	Ile	Lys	Ser	Glu	Met	Lys	Thr	Lys	Leu	Gly	Glu
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Gln	Gly	Pro	Gln	Ile	Leu	Ser	Val	Gln	Arg	Val	Tyr	Ile	Gln	Thr	Arg
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Glu	Glu	Lys	Arg	Ile	Asn	Leu	Thr	Ile	Gly	Ser	Arg	Ala	Tyr	Leu	Leu
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Pro	Asn	Thr	Ser	Val	Ile	Ile	Lys	Cys	Pro	Val	Arg	Arg	Phe	Gln	Lys
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Pro	Ala	Leu	Arg	Glu	Pro	Met	Arg	Glu	Tyr	Pro	Gly	Met	Asp	His	Ser
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<212> DNA

<213> Homo sapiens

<400> 529

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<211> 802

<212> PRT

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 532

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<213> Homo sapiens

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Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
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115

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<212> DNA

<213> Homo sapiens

<400> 539

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 ttacttgcca tttatggaaa aaaggggggat acaagcaaca tcatcacagt aagagtggct
 180
 gatgggcaaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
 240
 attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac
 300
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa
 360
 gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac
 420
 tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttcta
 480
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa
 534

<210> 540

<211> 143

<212> PRT

<213> Homo sapiens

<400> 540

Xaa	Arg	Val	Lys	Lys	Lys	Lys	Met	Lys	Glu	Ser	Glu	Ala	Asp	Ser	Glu
1			5					10					15		
Val	Lys	His	Gln	Pro	Ile	Phe	Ile	Lys	Glu	Arg	Leu	Lys	Leu	Phe	Glu
			20					25					30		
Ile	Leu	Lys	Lys	Asp	His	Gln	Leu	Leu	Leu	Ala	Ile	Tyr	Gly	Lys	Lys
			35				40					45			
Gly	Asp	Thr	Ser	Asn	Ile	Ile	Thr	Val	Arg	Val	Ala	Asp	Gly	Gln	Thr
			50			55					60				
Val	Gln	Gly	Glu	Val	Trp	Lys	Thr	Thr	Pro	Tyr	Gln	Val	Ala	Ala	Glu
65					70				75					80	
Ile	Ser	Gln	Glu	Leu	Ala	Glu	Ser	Thr	Val	Ile	Ala	Lys	Val	Asn	Gly
			85					90					95		
Glu	Leu	Trp	Asp	Leu	Asp	Arg	Pro	Leu	Glu	Gly	Asp	Ser	Ser	Leu	Glu
			100					105					110		
Leu	Leu	Thr	Phe	Asp	Asn	Glu	Glu	Ala	Gln	Ala	Val	Ser	Ile	Leu	Lys
			115				120					125			
Pro	Asp	Ser	Gln	Thr	Leu	Gly	Ser	Tyr	Val	Val	Asn	Tyr	Ile	Ile	
			130				135					140			

<210> 541

<211> 551

<212> DNA

<213> Homo sapiens

<400> 541

ggtaccgagc tgcgcgtgtg gstatgcgcc ttctatgcca agaagatgga caagcccatg
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ctgaagcagg ccggctctgg cgtccacgct gcaggcacc cagaaaacag cgcctccgtg
120
gagtcggagc ccagccagt ggcgtgtaaa gtgtgttctg ccaccttctt ggagctgcag
180
ctcctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactcct gtgtcgattt
240
ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgtcctg
300
tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct
360
tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcactcctca ctctctctgg
420
ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
480
caggagccag ccgtggcatg tgttgtgcac tcttgccctt gttgtctcta cttgacagcc
540
ccctcacgcg t
551

<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

Met	Asp	Lys	Pro	Met	Leu	Lys	Gln	Ala	Gly	Ser	Gly	Val	His	Ala	Ala
1				5					10					15	
Gly	Thr	Pro	Glu	Asn	Ser	Ala	Pro	Val	Glu	Ser	Glu	Pro	Ser	Gln	Trp
			20					25						30	
Ala	Cys	Lys	Val	Cys	Ser	Ala	Thr	Phe	Leu	Glu	Leu	Gln	Leu	Leu	Asn
			35					40					45		
Gly	Lys	Glu	Asp	Val	Trp	Gly	Ala	Pro	Val	Val	Lys	Leu	Leu	Cys	Arg
			50					55				60			
Phe	Leu	Ser	Asp	Leu	Arg	Cys	His	Leu	Ser	Ala	Ala	Val	Gly	Gly	Val
65					70					75					80
Pro	Asp	Phe	Val	Leu	Ser	Ala	Pro	Leu	Pro	His	Asn	Val	Val	Ala	Arg
				85						90				95	
Thr	Lys	Ala	Phe	Ser	Gly	Phe	Lys	Ala	Ser	Gly	Gln	Ser	Arg	Phe	Pro
			100					105						110	
Pro	Pro	Thr	Pro	Ala	Gly	Leu	Thr	Pro	His	Ser	Ser	Trp	Leu	Gly	Ser
			115					120					125		
Cys	Ile	Ser	Ala	Gly	Arg	Leu	Asp	Ser	Gly	Ala	Leu	Ala	Gly	Ala	Arg
			130					135					140		
Gly	Gln	Glu	Pro	Ala	Val	Ala	Cys	Val	Val	His	Ser	Cys	Leu	Cys	Cys
145					150					155					160
Leu	Tyr	Leu	Thr	Ala	Pro	Ser	Arg								
					165										

<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
 nnaagccgg acatgaatac ccgcattgct ggcaaaactg tcctgaccat cattctggcc
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 gggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg
 120
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
 240
 gggcgctcct gggatctgga ccgcaccgcg ggtggcctga aggtcatgcc gcccttttcc
 300
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt
 349

<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
 1 5 10 15
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
 115

<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca
 60
 caagaaattg ttggtgtcat cacagggttct gcaatgccgg gtgggttcagc aaaccgtatc
 120
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
240
gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat
300
acgttatata cctataaaat ggaaagttca ttagtgaaac aagtgcctga agatgcaatg
360
ctatttgctt tgggtcccc ccccccccc
390

<210> 546
<211> 130
<212> PRT
<213> Homo sapiens

<400> 546
His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
1 5 10 15
Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
20 25 30
Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
35 40 45
Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
50 55 60
Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala
65 70 75 80
Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
85 90 95
Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val
100 105 110
Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
115 120 125
Pro Pro
130

<210> 547
<211> 306
<212> DNA
<213> Homo sapiens

<400> 547
aagcttggtt ttctgatttt tattcaaata tctatcatgg atgaagcatg cagtttcaga
60
atcagttcag tggtgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
120
gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
180
cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
240
tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnncenn
300
nnccnn
306

<210> 548

<211> 90
 <212> PRT
 <213> Homo sapiens

<400> 548
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1 5 10 15
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
 20 25 30
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
 35 40 45
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50 55 60
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
 65 70 75 80
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa
 85 90

<210> 549
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 549
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttggttaat
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 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatttc
 120
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca
 180
 tgttattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
 240
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
 300
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
 360
 aagattttcta aggatgcagg gatgcccac cagggccagc catgcttctg caaatatgca
 420
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
 480
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
 540
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca
 600
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat
 660
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
 720
 gccgatgtca ctcatccacc tgctgggtgat ggaaagaagc cttctattgc tgctgttgta
 780

<210> 550
 <211> 192
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
           20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
           35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
           50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
           85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
           100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
           115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
           130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
           165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
           180          185          190

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<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gtcggttgcc
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gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtcct cgtcgtcaat cgcaccgggc cgcggggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggcg ctgaccgatg cgcccatcgg cgggctcatc tggctggcgc
240
tagcgggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

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<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

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          20          25          30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala
          35          40          45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
          50          55          60
Ser Gly Arg
65

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<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

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<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
ggtgttggtt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc gggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgttttaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

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<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

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<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
1          5          10          15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
          20          25          30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
          35          40          45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
          50          55          60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65          70          75          80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
          85          90          95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
          100          105          110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
          115          120          125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

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130	135	140
Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg		
145	150	155

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 555
 tctagagatt gagaacaatt atggatacag aaatgggtga ttccgtcaaa tatattcgag
 60
 attcggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
 120
 tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
 180
 ttaataaagt acctagaatt gtctgcctgc ttctccggct tagtgtgttc gtcgctgcgg
 240
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
 300

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 556
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1 5 10 15
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
 20 25 30
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
 35 40 45
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
 50 55 60
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
 65 70 75 80
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
 85 90

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 557
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
 60
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac
 120
 gtgttcccgg ctaccacta tgctgccggc ccggaacgta tggagcgggc catagcgtcc
 180
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcgggtgcc
 300
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctcagccccg
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg
 420
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
 480
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcggg tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
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Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
	35						40				45				
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
	50					55					60				
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65				70					75					80	
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
			85						90					95	
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
			100						105				110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
			115					120				125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
	130					135					140				
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145					150				155					160	
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
			165						170					175	
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
			180					185					190		
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
	195						200					205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
	210					215					220				
Thr	Arg														
225															

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
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 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgta tccaggagct gaagccctta atcagctagg gtcacacag agtcaaggta
 300
 gggtaaaaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
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 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat
 300

gacccctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggcagcgcct gggagggttat cggaccagtg ctgtggcctc
 420
 aggcctgcaa tttgatgttg aaaccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 562
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1 5 10 15
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
 20 25 30
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
 35 40 45
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
 50 55 60
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro
 65 70

<210> 563
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 563
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 60
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga
 120
 aaaggaaggg aaaaggcctc aaccttggcc agggctggaa cccacaggag gccagggtag
 180
 ggggcagacg gatggcagca gcactgcctg agagtgggg gagctccac ggggcagcaa
 240
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggctgccc
 300
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 564
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1 5 10 15
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

20						25						30			
Thr	Gly	Asn	Ala	His	Pro	Lys	Lys	Arg	Lys	Gly	Lys	Gly	Leu	Asn	Leu
35						40						45			
Gly	Gln	Gly	Trp	Asn	Pro	Gln	Glu	Ala	Arg	Val	Arg	Gly	Arg	Arg	Met
50						55						60			
Ala	Ala	Ala	Leu	Pro	Glu	Ser	Trp	Gly	Ser	Ser	His	Gly	Ala	Ala	Ser
65						70						75			
Gly	Gly	Gln	Arg	Val	Trp	Pro	Ser	Ala	Leu	Val	Ser	Val	Thr	Thr	Val
85						90						95			
Gly	Leu	Pro	Ala	Pro	Pro	Leu	His	His							
100						105									

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<210> 565
<211> 311
<212> DNA
<213> Homo sapiens
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<400> 565
nctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccacca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctcctcctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttggggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311
```

```
<210> 566
<211> 101
<212> PRT
<213> Homo sapiens
```

```

<400> 566
Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
 1          5          10          15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
          20          25          30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
          35          40          45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
 50          55          60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65          70          75          80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
          85          90          95
Ala Gln Glu Ala Pro
          100

```

<210> 567
<211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcaccttgtc gaaatattca tccttgagat
 60
 cagcccacgt gccgtcgacc tctacctcgg tgaggggtgc gggcgggtac caacagccga
 120
 cctcgtcctc ggctccactc atggcggcaa gtcccgctgc cagtccgggg atcgtcgggg
 180
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgcgcacgca
 240
 cggatatcagt gccgcagtaa tagagggtc gcatgaattc gaccggacaa tccagttgga
 300
 ggcagtccea ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgctcg gtgagcggac
 420
 gctcccgatc cccgcccgga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcggtg cacttcgcgg tcgccgcggt tctacgatgt tggcatgccg
 540
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaaccgat
 600
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
 660
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggatcaca actctcgggt gagcgggtga ttacatgcc cagccgctgt gaacggccca
 780
 tcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cacgtggtca ggggtggggc
 900
 caccacacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro
 1 5 10 15
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu
 20 25 30
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp
 35 40 45
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr
 50 55 60
 His Asn Ser Arg Val Ser Gly
 65 70

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtag ttgatttagt ggcctttaac aaaacgctac
 120
 ctgtcgatta cttaatgggc gaaggaacgg aacttggtga ttcaaactg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcggtatg tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
 nacgcgtatc ttcgctgggc cacaccagac gtggcattaa acgacgtcac aagaacgaca
 60
 ccgggccttg acgggcccac gcacgaagag gccaagacac tgaccgagac tactgtttcc
 120
 gttcccaccc ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgaattgc cgtcgagggc
 240
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc
 300
 atcttgacgc gcatcaccct gcccgggtgac gaagggttggg aagaactcac caccaaaggc
 360
 aagcccccaa gcactcgtga tgtgccccta cccgggagct aggtcgg
 407

<210> 572

<211> 100

<212> PRT

<213> Homo sapiens

<400> 572

Leu	Thr	Glu	Thr	Thr	Val	Ser	Val	Pro	Thr	Ser	Phe	Ala	Asp	Leu	Gly
1				5					10					15	
Val	Arg	Glu	Asp	Ile	Cys	Gln	Ala	Leu	Glu	Gly	Val	Gly	Ile	Val	Ser
			20					25						30	
Pro	Phe	Pro	Ile	Gln	Ala	Met	Ser	Ile	Pro	Ile	Ala	Val	Glu	Gly	Thr
			35				40					45			
Asp	Leu	Ile	Gly	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Leu	Ala	Phe
	50					55				60					
Gly	Ile	Thr	Ile	Leu	Gln	Arg	Ile	Thr	Leu	Pro	Gly	Asp	Glu	Gly	Trp
65					70					75					80
Glu	Glu	Leu	Thr	Thr	Lys	Gly	Lys	Pro	Pro	Ser	Thr	Arg	Asp	Val	Pro
				85				90						95	
Leu	Pro	Gly	Ser												
			100												

<210> 573

<211> 393

<212> DNA

<213> Homo sapiens

<400> 573

acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacaccac gcagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
 300
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574

<211> 124

<212> PRT

<213> Homo sapiens

<400> 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
      20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
      35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
      50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
      65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
      85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
      100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
      115          120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

```

nntatccatg cagacatggg accaggggtct ctgaggggcag gaagcaaagt gggtgagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttcagg gcctcaggga
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatgggcccgt
372

```

<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
      20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
      35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

<210> 577
 <211> 432
 <212> DNA
 <213> Homo sapiens

```

<400> 577
nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggtat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccgt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgcg
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacgggtt tcggatcatc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 578
Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 579
 ggccccaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc
 60
 ctgctcccag ggatcaccac cttaccacagc gggccacctg ctcccccggt ccccgcggcg
 120
 cccggcccct ggctgcgcag acccctcttc agcctgaagc tgtccgacac agaggacgtc
 180
 ttctctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtgtt cgtgcaggcg
 240
 gccttgcccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
 300
 tcttcacgcc cggccccggg
 320

<210> 580
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
 1 5 10 15
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
 20 25 30
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
 35 40 45
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
 50 55 60
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
 65 70 75 80
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
 85 90 95

<210> 581
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 581
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc
 60
 cacgtcggca tgggcttcaa gacgccagta cgcattgcaca gcgtcgaccc caagaccgcg
 120
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac
 180
 accaagcagc tgaccggcga cctgggtttc tccgggtttca agctgttcaa ggcgccggaa
 240

ctggatcgcc atgacgtgct gtcgtttctc ggccgagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 582
 Xaa Asp Gly Asn His Ser Leu Trp Lys Glu Leu Asn Gly Gln Leu Asp
 1 5 10 15
 Val Gln Phe Phe His Val Gly Met Gly Phe Lys Thr Pro Val Arg Met
 20 25 30
 His Ser Val Asp Pro Lys Thr Arg Glu Ala Arg Glu Val His Phe Arg
 35 40 45
 Pro Ser Leu Phe Asn Tyr Ala Lys Thr Thr Val Asp Thr Lys Gln Leu
 50 55 60
 Thr Gly Asp Leu Gly Phe Ser Gly Phe Lys Leu Phe Lys Ala Pro Glu
 65 70 75 80
 Leu Asp Arg His Asp Val Leu Ser Phe Leu Gly Ala Ser Tyr Phe Arg
 85 90 95
 Ala Val Asp Ala Thr Arg Gln Tyr Gly Leu Ser Ala Arg Gly Leu Ala
 100 105 110
 Ile Asp Thr Tyr Ala Lys Lys Arg Glu Glu Phe Pro Asp Phe Thr Gln
 115 120 125
 Phe Trp Phe Glu Thr Pro Ser Lys Asp Pro Arg
 130 135

<210> 583
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 583
 cttttgatca atgctgatgg cacgaagcta tcgaaaaggt cgggtgatgt ccgcgtagct
 60
 gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc
 120
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcg cgtcgtaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 584
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1 5 10 15
 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
 20 25 30
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
 35 40 45
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
 50 55 60
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
 65 70 75 80
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
 85 90 95
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
 100 105 110
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
 115 120 125
 Val Thr Leu Gly Pro Gln Arg
 130 135

<210> 585
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 585
 nnacgcgtcc tcgctggata tgaggctgtg aagagggaac gctgcgtcat tgatctggac
 60
 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
 120
 cgggctcggg accgacattt cgttgctcgac gaataccagg acgtttctcc gctgcagcat
 180
 aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
 240
 caggccattc actcttatgc aggcgcacga gctgactacc tctcgcactt cgttgccgat
 300
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcgtt
 360
 cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
 420
 aggggagtca cattgggttc gcggggtcga tccgggtccg agcccatcta tcaggctctc
 480
 ggggacgatg cctccgaagc tt
 502

<210> 586
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 586

Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
 1 5 10 15
 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
 20 25 30
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
 35 40 45
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
 50 55 60
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
 65 70 75 80
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
 85 90 95
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
 100 105 110
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
 115 120 125
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
 130 135 140
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
 145 150 155 160
 Gly Asp Asp Ala Ser Glu Ala
 165

<210> 587

<211> 746

<212> DNA

<213> Homo sapiens

<400> 587

gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
 60
 gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcccga
 120
 tgccctgcagc gctctgaccc ggccctctac gggggtgtcc aggccgcctt ccctggcgcc
 180
 ttcagcttcc gccatgctgc ggggttctctg tgccactgcc ctcttggtt tgagggagcc
 240
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
 300
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
 360
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgac
 420
 actgtggcag gctatatctg caggtgccc gagacctggg gtgggcgcga ctgttctgtg
 480
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
 540
 gagtctgggg tccacagtta cgtctgccac tgcccactg gtacccatgg accgttctgt
 600
 ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct
 660
 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgtgg gaccttggcc
 720

actcgcaatg acaccaagga aagctt
746

<210> 588
<211> 248
<212> PRT
<213> Homo sapiens

<400> 588
Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro
1 5 10 15
Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
20 25 30
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
35 40 45
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
50 55 60
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
65 70 75 80
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
85 90 95
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
100 105 110
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
115 120 125
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
130 135 140
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
145 150 155 160
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
165 170 175
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
180 185 190
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
195 200 205
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
210 215 220
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
225 230 235 240
Thr Arg Asn Asp Thr Lys Glu Ser
245

<210> 589
<211> 381
<212> DNA
<213> Homo sapiens

<400> 589
atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag
60
ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgtaaat
120
gtgggttggtg taacttcagc tttagggtcag cagccttcca tttccagttt ggctcaaccc
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc
 300
 catgtcaaat cagtgactca aaatcctgct tcagagtatg tacaacagca gccaatctt
 360
 caaacagcaa tgcctccgg a
 381

<210> 590
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 590
 Ile Ser Gln Val Gln Leu Gln Ser Gln Glu Leu Ser Tyr Gln Gln Lys
 1 5 10 15
 Gln Gly Leu Gln Pro Val Pro Leu Gln Ala Thr Met Ser Ala Ala Thr
 20 25 30
 Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu
 35 40 45
 Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr
 50 55 60
 Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro
 65 70 75 80
 Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln
 85 90 95
 Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu
 100 105 110
 Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly
 115 120 125

<210> 591
 <211> 684
 <212> DNA
 <213> Homo sapiens

<400> 591
 tcgaccatgg atcatctgcg ccacggcatc cacctgcgtg gttatgcgca gaagaaccg
 60
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 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg
 540
 gtccttggcc tacgttgacac ccggttgccg gttttgaact cggatcgcgc tcggccggta
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<210> 592
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 592
 Ser Thr Met Asp His Leu Arg His Gly Ile His Leu Arg Gly Tyr Ala
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 20 25 30
 Ser Glu Leu Leu Asp Ser Ile Lys Arg Asp Ser Ile Arg Val Leu Phe
 35 40 45
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg
 50 55 60
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His
 65 70 75 80
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val
 85 90 95
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly
 100 105 110
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys
 115 120 125
 His Gly Gln Ile Ser
 130

<210> 593
 <211> 615
 <212> DNA
 <213> Homo sapiens

<400> 593
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 gataccatcc ccgcgccgct aggccagcca cgatggtcga cggccaccat ccagacccca
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 gtcataccta ctacacgtgg tcgattcgtg atcggccccg tcatgatgcg caccatcgac
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 ccgtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcacg
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 ccaaggatcg tcgatttggg cgcctccggg gagctcgggg gtcagggatt cgacacaagg
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 420

accggagact cgggtgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg
 480
 gtccgatgcg aggagcaggc ctggaaccca tccgtcgtca tcgtgttgga ttctcgggct
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<210> 594
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 594
 Xaa Arg Val Gln Thr Ala Arg Ser Leu Ala Pro Val Arg Ile Ala Leu
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 Gly Ser Gln Thr Cys Glu Thr Val Thr Val Glu Arg Arg Gly Gly Leu
 20 25 30
 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly
 35 40 45
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr
 50 55 60
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp
 65 70 75 80
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu
 85 90 95
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu
 100 105 110
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg
 115 120 125
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser
 130 135 140
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met
 145 150 155 160
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu
 165 170 175
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe
 180 185 190
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg
 195 200 205

<210> 595
 <211> 303
 <212> DNA
 <213> Homo sapiens

<400> 595
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 120
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 180

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<210> 596
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 596
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 20 25 30
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
 35 40 45
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
 50 55 60
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp
 65 70 75 80
 Asp Gln Gly Pro Arg Asp Leu Val
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<210> 597
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 597
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 aagaaccaca tgggtggagaa gacctacgaa tgtaaagaat gcgggaaatc ctttggcgat
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 ctcgtgtccc ggaggaaaca catgaggatt cacatcgtca agaaaccgt ggaatgtcgg
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 240
 ggagagaaac catacgggtg cgatctctgc gggaaagctt tcagcgcgag ttcaaacctc
 300
 accgcacaca ggaagataca cagcaagag agacgctacg aatgcgccgc ctgcgggaaa
 360
 gtcttcggtg actatttatc ccggcggagg cacatgagcg ttcaccttgt aaagaaacga
 420
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 660

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1260
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1440
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2280

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 2460
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 2520
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 2580
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 2700
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 2709

<210> 598
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 598
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 Asn Leu His Lys Lys Asn His Met Val Glu Lys Thr Tyr Glu Cys Lys
 20 25 30
 Glu Cys Gly Lys Ser Phe Gly Asp Leu Val Ser Arg Arg Lys His Met
 35 40 45
 Arg Ile His Ile Val Lys Lys Pro Val Glu Cys Arg Gln Cys Gly Lys
 50 55 60
 Thr Phe Arg Asn Gln Ser Ile Leu Lys Thr His Met Asn Ser His Thr
 65 70 75- 80
 Gly Glu Lys Pro Tyr Gly Cys Asp Leu Cys Gly Lys Ala Phe Ser Ala
 85 90 95
 Ser Ser Asn Leu Thr Ala His Arg Lys Ile His Thr Gln Glu Arg Arg
 100 105 110
 Tyr Glu Cys Ala Ala Cys Gly Lys Val Phe Gly Asp Tyr Leu Ser Arg
 115 120 125
 Arg Arg His Met Ser Val His Leu Val Lys Lys Arg Val Glu Cys Arg
 130 135 140
 His Cys Gly Lys Ala Phe Arg Asn Gln Ser Thr Leu Lys Thr His Met
 145 150 155 160
 Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Asp His Cys Gly Lys
 165 170 175
 Ala Phe Ser Ile Gly Ser Asn Leu Asn Val His Arg Arg Ile His Thr
 180 185 190
 Gly Glu Lys Pro Tyr Glu Cys Leu Val Cys Gly Lys Ala Phe Ser Asp
 195 200 205
 His Ser Ser Leu Arg Ser His Val Lys Thr His Arg Gly Glu Lys Leu
 210 215 220
 Phe Xaa Cys His Pro Cys Gly Lys Gly Ser Ser Glu Arg Ala Xaa Leu
 225 230 235 240

<210> 599
<211> 340
<212> DNA
<213> Homo sapiens

<400> 599
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gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta
240
tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc
300
caccggcgca tgggtgtcca gatcgtccag ggcgatgatca
340

<210> 600
<211> 111
<212> PRT
<213> Homo sapiens

<400> 600
Met Pro Trp Thr Ile Trp Ser Thr Ile Ala Gly Trp Asn Thr Pro Ser
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Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His
20 25 30
Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
35 40 45
Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
50 55 60
Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
65 70 75 80
Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
85 90 95
Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
100 105 110

<210> 601
<211> 421
<212> DNA
<213> Homo sapiens

<400> 601
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ccgcgctcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccg
120
cagctgtcga tggccccgct gtctatcggg aatctgcaat cggtaggacgt ggtgcgcggc
180
ggcggcgcgg tgcgctacgg gccgcagaac gtcggcggcg tgatcaactt cgttaccgga
240

gacattccca aaacgtttgg cggtgccgcc agcgtacaaa cccaggggtgc cagccacggc
300
ggcctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc
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gagctgctct actccggcct gcacggccag ggctaccgag acaacaacga caacaccgac
420
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421

<210> 602
<211> 140
<212> PRT
<213> Homo sapiens

<400> 602
Ala Gly Gly Ser Asp Ile Ser Leu Asn Val Gly Val Arg Gly Leu Thr
1 5 10 15
Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu
20 25 30
Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser
35 40 45
Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val
50 55 60
Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg
65 70 75 80
Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly
85 90 95
Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly
100 105 110
Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His
115 120 125
Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp
130 135 140

<210> 603
<211> 309
<212> DNA
<213> Homo sapiens

<400> 603
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ttcgacggcc tggccatcgg cggtctgtcg gtgggcgagc ccaagcacga gatgatcaag
120
gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcggt
180
ggcaaaccgg aagacctcgt agaggggtgtg cgccgcgggtg tggacatgtt cgattgcgtg
240
atgccaaccc gtaatgcccg caatgggcat ctgttcacg atacaggcgt gctgaagatc
300
cgtaacgag
309

<210> 604

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 604
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu
 1 5 10 15
 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
 20 25 30
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
 35 40 45
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
 50 55 60
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
 65 70 75 80
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
 85 90 95
 Val Leu Lys Ile Arg Asn Ala
 100

<210> 605
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 605
 acgcgttcac gatagggtag ttgcctatatt caacgcggtc ggtattttcc tgcacaacaa
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 actggcccaa ggctgggcta tagtcagggtg catagtactt ggtgaagtag cgtacgtccg
 120
 caccacatc acatttcagt accttggtta tcttcaatcg gaaaaaaga ttggagtaaa
 180
 tggtgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg
 240
 attcccagtg caaaggtccc catgctacat cctgcgacaa tgaggccgtt agcacgttta
 300
 ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgtgatac tgattgttga
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 tggatataggc ttgcgccagg taggtataat tgggtcaattc gtccatggca atgcgcagtg
 420
 aagtcttg
 428

<210> 606
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 606
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile
 1 5 10 15
 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser
 20 25 30
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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      35      40      45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
      50      55      60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
65      70      75      80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85      90      95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100      105      110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115      120      125
Asn Tyr Pro Ile Val Asn Ala
      130      135

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<210> 607
 <211> 366
 <212> DNA
 <213> Homo sapiens

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<400> 607
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120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
240
acaacgcacg gtgtgtacaa cgtgttcacc aacagcttcc attcgagctg tccatttttg
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gacgcg
366

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<210> 608
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
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Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
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Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
35      40      45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
50      55      60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
65      70      75      80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
85      90      95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
 115 120
 <210> 609
 <211> 291
 <212> DNA
 <213> Homo sapiens
 <400> 609
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 cctggaccat ctggggcggg ggcgccgccc tgggtggaggc ggggtggagcc g
 291

<210> 610
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 610
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp
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 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
 20 25 30
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
 35 40 45
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
 50 55 60
 Trp Arg Val Glu Pro
 65

<210> 611
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 611
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 tgtacccaag tagagaggtg ttcgatgccca cacagtccgg aagaaaagaa gcaagcactg
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 acgcgcacatca ggcgcatcaa aggtcaggta gcgactcttg agcaagcgct tgatgcagg
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 gcgaaatgtc ctgcaattct tcagcagctt gcggccgttc gtggcgagc caacggattg
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gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
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 aggcaccagg gtgtcctcgg tgagggcaaa ttt
 393

<210> 612
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 612
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys
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 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser
 20 25 30
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly
 35 40 45
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro
 50 55 60
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu
 65 70 75 80
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser
 85 90 95
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser
 100 105 110
 Ile Val Arg Ser Tyr Leu Arg
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<210> 613
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 613
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 aactggata aagagagtgg agaaagcctc agagtttgca gtgtcaaag cattttttac
 180
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga
 240
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggt
 300
 agacaccaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
 360
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga
 420
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 540
 ccaagacaag aagcagcaga aggatcc
 567

<210> 614
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 614
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly
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 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
 20 25 30
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
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 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
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 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
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 <212> DNA
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 Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser
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 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu
 65 70 75 80
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 85 90 95
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu
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 115 120 125
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 130 135 140
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile
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 Arg Leu His Ser Ser
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 <212> DNA
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<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

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<212> DNA

<213> Homo sapiens

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 35 40 45
 Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
 50 55 60
 His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
 65 70 75 80
 Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
 85 90 95
 Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
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      35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
      50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
      85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
      100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
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<211> 345

<212> DNA

<213> Homo sapiens

<400> 623

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<211> 111

<212> PRT

<213> Homo sapiens

<400> 624

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Gly Thr Ile Ala Gln Ala Glu Asp Leu Pro Pro Asp Asp Thr His Thr
      35           40           45
Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
      50           55           60
Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly

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35 40 45
Ala Gln Cys Lys Gly Arg Gln Thr Cys Trp Ser Leu Gly Tyr Asp Pro
50 55 60
Glu Gln Ser Gly Gly Ala Glu Ser Ser Cys Leu Trp Ala Ser Ile Ala
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<212> PRT

<213> Homo sapiens

<400> 628

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<213> Homo sapiens

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Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
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Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
      65           70           75           80
Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
      85           90           95
Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
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 Val Asp Ala Val Val Asn Ala Val Glu His Tyr Ser Glu Leu Thr Pro
 35 40 45
 Gln Leu Leu Thr Thr Gly Gly Thr Ser Asp Gly Arg Phe Ile Ala Gln
 50 55 60
 Met Gly Xaa Gln Val Val Glu Leu Gly Pro Val Asn Ala Thr Ile His
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<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
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Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
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Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
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His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
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Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
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Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
			165						170					175	
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
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Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
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Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
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Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
			245						250					255	
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg
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Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
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Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

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Ser Met Ser Asp Leu Tyr	Asp Met Gln Lys Arg	Gln Arg Gln His Arg
305	310	315
His Arg Asn Gln Ser Gly	Ala Thr Thr Ser Ser	Gly Asp Thr Glu Ser
325	330	335
Glu Glu Gly Glu Gly Glu	Thr Thr Val Arg Leu	Leu Trp Leu Ser Met
340	345	350
Leu Lys Met Pro Arg Glu	Leu Met Arg Leu Cys	Leu Cys His Leu Leu
355	360	365
Thr Trp Phe Ser Val Ile	Ala Glu Ala Val Phe	Tyr Thr Asp Phe Met
370	375	380
Gly Gln Val Ile Phe Glu	Gly Asp Pro Lys Ala	Pro Ser Asn Ser Thr
385	390	395
Ala Trp Gln Ala Tyr Asn	Ala Gly Val Lys Met	Gly Cys Trp Gly Leu
405	410	415
Val Ile Tyr Ala Ala Thr	Gly Ala Ile Cys Ser	Ala Leu Leu Gln Lys
420	425	430
Tyr Leu Asp Asn Tyr Asp	Leu Ser Val Arg Val	Ile Tyr Val Leu Gly
435	440	445
Thr Leu Gly Phe Ser Val	Gly Thr Ala Val Met	Ala Met Phe Pro Asn
450	455	460
Val Tyr Val Ala Met Val	Thr Ile Ser Thr Met	Gly Ile Val Ser Met
465	470	475
Ser Ile Ser Tyr Cys Pro	Tyr Ala Leu Leu Gly	Gln Tyr His Asp Ile
485	490	495
Lys Gln Tyr Ile His His	Ser Pro Gly Asn Ser	Lys Arg Gly Phe Gly
500	505	510
Ile Asp Cys Ala Ile Leu	Ser Cys Gln Val Tyr	Ile Ser Gln Ile Leu
515	520	525
Val Ala Ser Ala Leu Gly	Gly Val Val Asp Ala	Val Gly Thr Val Arg
530	535	540
Val Ile Pro Met Val Ala	Ser Val Gly Ser Phe	Leu Gly Phe Leu Thr
545	550	555
Ala Thr Phe Leu Val Ile	Tyr Pro Asp Val Ser	Glu Glu Ala Lys Glu
565	570	575
Glu Gln Lys Gly Leu Ser	Ser Pro Leu Ala Gly	Glu Gly Arg Ala Gly
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<211> 370

<212> DNA

<213> Homo sapiens

<400> 637

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<210> 638
<211> 99
<212> PRT
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35 40 45
Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly
50 55 60
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<210> 640
<211> 110
<212> PRT
<213> Homo sapiens

<400> 640

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Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
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Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
          35           40           45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
          50           55           60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
65           70           75           80
Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp
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Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
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<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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<210> 642

<211> 163

<212> PRT

<213> Homo sapiens

<400> 642

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          20           25           30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
          35           40           45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

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Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65      70      75      80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85      90      95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100      105      110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115      120      125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
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Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
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<210> 643
 <211> 628
 <212> DNA
 <213> Homo sapiens

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<210> 644
 <211> 209
 <212> PRT
 <213> Homo sapiens

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<400> 644
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Lys	Ser	Ser	Pro	Ser	Arg	Gln	Gly	Trp	Val	Ser	Pro	Ala	Tyr	Leu	Asp
	50		55		60										
Arg	Arg	Leu	Lys	Leu	Ser	Pro	Glu	Trp	Gly	Ala	Ala	Glu	Ala	Pro	Glu
65			70		75				80						
Phe	Pro	Gly	Glu	Ala	Val	Ser	Glu	Asp	Glu	Tyr	Lys	Ala	Arg	Leu	Ser
			85		90				95						
Ser	Val	Ile	Gln	Glu	Leu	Leu	Ser	Ser	Glu	Gln	Ala	Phe	Val	Glu	Glu
	100		105		110										
Leu	Gln	Phe	Leu	Gln	Ser	His	His	Leu	Gln	His	Leu	Glu	Arg	Cys	Pro
	115		120		125										
His	Val	Pro	Ile	Ala	Val	Ala	Gly	Gln	Lys	Ala	Val	Ile	Phe	Arg	Asn
	130		135		140										
Val	Arg	Asp	Ile	Gly	Arg	Phe	His	Ser	Ser	Phe	Leu	Gln	Glu	Leu	Gln
145			150		155									160	
Gln	Cys	Asp	Thr	Asp	Asp	Val	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln	
			165		170				175						
Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	Phe	Leu	Val	Gly	Arg	Val	Gln	Ala
			180		185				190						
Glu	Ser	Val	Val	Val	Ser	Thr	Ala	Ile	Gln	Glu	Phe	Tyr	Lys	Lys	Tyr
	195		200		205										
Ala															

<210> 645

<211> 417

<212> DNA

<213> Homo sapiens

<400> 645

atccataggc attgccagag tattcacttc ctgttgagg cacacagggg agaggcctgt
60gaggggaagg gcatcaatgc agggctgggg tgtgggaagg tctgcagggc tggcaatggg
120caagctcagg aatggtgggg gagacagttg gagccacggc agggacaatg gagctcagaa
180ggtcctctg tcatcccttt tggaacccat tgatctggaa aatttggggc agtgtccttt
240tccgtaggta ctggaggcac tggcttgaca tactacagcc ctcccaggag gccagaagg
300tagatgttat aactacccc attttccaga tgaagaaact gagcctctgg gatctgcgga
360agctcccaga gctggagcag ttagtcctg ggcctacac tcacagcaca gtttccc
417

<210> 646

<211> 95

<212> PRT

<213> Homo sapiens

<400> 646

Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

1	5	10	15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp			
20	25	30	
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu			
35	40	45	
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile			
50	55	60	
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu			
65	70	75	80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser			
85	90	95	

<210> 647

<211> 421

<212> DNA

<213> Homo sapiens

<400> 647

acgcgtttcg gttcttgagc gcttccacca attcagcggg ggtgagcggc ccctgtgcat
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cgcgagcag ggtgatcaga taggcgatat cgcctcgtt cagttgcacg gtgtcgttat
120
cggtagccat gcgtggcgaa ctcttttggc atgggaaaat cgggtgaggg caacggggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttccgccc
240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cacctgctac cgctcgggtg
300
tacgatagcc gcggcgccac cagggttggt acattccaaa cgcaacgcag gaaccgcgat
360
gaacagcgtt ttctgcaaca aacccttat gacgctggct ctggggcatt tcagtgtcga
420
c
421

<210> 648

<211> 90

<212> PRT

<213> Homo sapiens

<400> 648

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro			
1	5	10	15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe			
20	25	30	
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala			
35	40	45	
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr			
50	55	60	
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr			
65	70	75	80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg			
85	90		

<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
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 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc
 120
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
 180
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcggtga caagttccaa
 240
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttctgtc
 300
 tctctcgctc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtggaacc
 360
 aagcctagat tcgctgcaa gaaggccgac attttttaga cttgccacgt taaaggggac
 420
 tgcacaggca cgcactcaaa tcccccttc catgtcctcc gcctgtgcac attcaggcaa
 480
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
 563

<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1 5 10 15
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
 60
 cataatggag tccatgggggt caaagttatc tcctggagct cagcagttga tggatatggt
 120
 taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa
 180
 ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia
 240
 gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
 300
 cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
 351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5				10						15	
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
			20					25					30		
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
			35				40					45			
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
	50					55				60					
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65					70				75					80	
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
				85				90						95	

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccgggtg gggctggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
 60
 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgctca
 120
 cactcttctc ctggagaggg agcgagcccc caaatgttcc acactgtgtc cccagggccc
 180
 cctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggctcctggc
 240
 tcccttcccc cagaaccacc ctcagtttcc caggccttcc ccactctagc aggccctggg
 300
 gggcttttcc cccaagget tgetgaccca gtcccttctg ggggcagtag cagccccgt
 360
 ttcttcccaa ggggcaatgc cccctctcca gccccacct
 399

<210> 654

<211> 133
 <212> PRT
 <213> Homo sapiens

<400> 654
 Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1 5 10 15
 Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
 20 25 30
 Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
 35 40 45
 Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
 50 55 60
 Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
 65 70 75 80
 Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
 85 90 95
 Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
 100 105 110
 Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
 115 120 125
 Ser Pro Ala Pro Pro
 130

<210> 655
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 655
 tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
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 gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cggggttcaa gactcagcta
 120
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
 180
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
 240
 cttgacaaat gcaaggtgcc atacaaacag gaactgcaca atctcacgc ccggcctact
 300
 cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
 360
 ttgttttc
 368

<210> 656
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 656
 Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1 5 10 15
 Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

      20      25      30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
      35      40      45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
      50      55      60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
65      70      75      80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
      85      90      95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
      100      105

```

<210> 657

<211> 330

<212> DNA

<213> Homo sapiens

<400> 657

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gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaaccctg gggcgagtcc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cgggtgctgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga cccgcctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcctt
240
ggaccgcatg ggttgggacg tgccctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

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<210> 658

<211> 102

<212> PRT

<213> Homo sapiens

<400> 658

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Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
  1      5      10      15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
      20      25      30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
      35      40      45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
      50      55      60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
65      70      75      80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
      85      90      95
Trp Arg Ala Gly Gly Ala
      100

```

<210> 659

<211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tectcctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac
120
aaccccgta cctccgtgtt ccagtaagaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtectgggtg ccattggcct cctggtatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcagggtcttt gtgcaattgc tggagtgtct
420
gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tgggtgcagac tgttcagacc aggtacacat ttgggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt gggggtgtga tgatgtgcat cgcctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgccata agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta tecttccaag
780
cacgactatg tgtaatgtc taagacctc cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaate ctctatttct ttttttaaata ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact cccctcttc ctctagtca
1140
ataaacccat tgatgatcta tttccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttgaggc aaccaaact ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagtt tectgagctc tccactggag tctccccct ctgtcgtctt ctgcagcgg
1500

taccc
1505

<210> 660
<211> 261
<212> PRT
<213> Homo sapiens

<400> 660
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35 40 45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115 120 125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130 135 140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255
Lys His Asp Tyr Val
260

<210> 661
<211> 451
<212> DNA
<213> Homo sapiens

<400> 661
nnacgcgtgt agtttgtgta tcggcgcgga actcgccgct tctgatctcg aggagcttcc
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cccatggacg agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat
120

gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaaa ggggtggatcc
 180
 acccgtgagg ccaagcgcac ctgtgagtc tgtgaggtcc gccaggagt cttggagtac
 240
 gcccttgcca atgacgagag gtccggaatc tggggcggat tgtccgagat ggagaggcgt
 300
 cggctgcgca agcgggcgtg acctgacgtc ggagcgcggt tattgacacg gcccggtaaa
 360
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atgcgagacg
 420
 tgggtgtgcat cccgtgctcc atgacgtcga c
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
			35				40					45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
	50					55				60					
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65					70				75					80	
Leu	Arg	Lys	Arg	Ala											
				85											

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

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 ccctacgacg tgctcgtcgt aggggcgggt cccgccggtg ccgcggccgc cgtgtacgcg
 120
 gctcgtaagg gcattcgac cgccatggtc gggctctcga tcggcggcca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgcg tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
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 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcgggcg
 360
 cgctcagtca tcgtggccac cggtgcccgc tggcgcaacc ttggcgtacc tggcgaggag
 420
 gaataccgca ccaaggggtg gacctactgc ccgcactgcg atggcccgtc attcacaggc
 480

aaaaaggtgg ccgtcgtcgg aggtggaaac tccggtattg aggcgctat cgacctcgcc
 540
 ggcgtcgtcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
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 acacgtctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
 120
 cgctcacgcg gtggccccgg ccagcggctt ttccaggatc tcgaaacgca ggtcgtcgcg
 180
 cttggggatg ccgaatcgtt cgtcgccata cgggaacggc ttcttgatgc cggtgcgag
 240
 gtageccgcg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctgca
 300
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
 352

<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
 1 5 10 15
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
 20 25 30
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 667
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 cgggagatct ttgaatctct cggcccgggtg ctcgacaaga atccgcagta cgtggaggca
 120
 gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt
 180
 gacgacgagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatatc gtcggtactg
 240
 gggccgtata aggggtggatt gcgattccac ccctcggtgt acttaggaac gattaagttc
 300
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcggaag
 360
 ggtgggtcgg actttgatcc ccatgacgcg t
 391

<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
 1 5 10 15
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

35	40	45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly		
50	55	60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu		
65	70	75
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly		
85	90	95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr		
100	105	110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His		
115	120	125
Asp Ala		
130		

<210> 669
 <211> 707
 <212> DNA
 <213> Homo sapiens

<400> 669
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<210> 670
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 <212> PRT
 <213> Homo sapiens

<400> 670
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      50      55      60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
      65      70      75      80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85      90      95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100      105      110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115      120      125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130      135      140
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<210> 671

<211> 444

<212> DNA

<213> Homo sapiens

<400> 671

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<210> 672

<211> 103

<212> PRT

<213> Homo sapiens

<400> 672

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Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

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Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
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 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
      50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
  65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
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120

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<213> Homo sapiens

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<210> 676

<211> 2518

<212> PRT

<213> Homo sapiens

<400> 676

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783

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Ala Ala Ala Ser Glu Glu Ala Ala Phe Pro Pro Val Val Glu Asp Glu		
690	695	700
Glu Met Glu Ala Ser Gly Val Ser Gly Asn Glu Glu Glu Met Val Glu		
705	710	715
Glu Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu		
725	730	735
Cys Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile		
740	745	750
Pro Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro		
755	760	765
Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro		
770	775	780
Thr Pro Pro Arg Arg Thr Ser Arg Ala Pro Ile Glu Pro Thr Pro Ala		
785	790	795
Ser Glu Ala Thr Gly Ala Pro Thr Pro Pro Pro Ala Pro Pro Ser Pro		
805	810	815
Ser Ala Pro Pro Pro Val Val Pro Lys Glu Glu Lys Glu Glu Glu Thr		
820	825	830
Ala Ala Ala Pro Pro Val Glu Glu Gly Glu Glu Gln Lys Pro Pro Ala		
835	840	845
Ala Glu Glu Leu Ala Val Asp Thr Gly Lys Ala Glu Glu Pro Val Lys		
850	855	860
Ser Glu Cys Thr Glu Glu Ala Glu Glu Gly Pro Ala Lys Gly Lys Asp		
865	870	875
Ala Glu Ala Ala Glu Ala Thr Ala Glu Gly Ala Leu Lys Ala Glu Lys		
885	890	895
Lys Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala		
900	905	910
Pro Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp		
915	920	925
Glu Ala Glu Gly Gly Asp Lys Asn Arg Leu Leu Ser Pro Arg Pro Ser		
930	935	940
Leu Leu Thr Pro Thr Gly Asp Pro Arg Ala Asn Ala Ser Pro Gln Lys		
945	950	955
Pro Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala Ala Ala Ile Pro Pro		
965	970	975
Ile Gln Val Thr Lys Val His Glu Pro Pro Arg Glu Asp Ala Ala Pro		
980	985	990
Thr Lys Pro Ala Pro Pro Ala Pro Pro Pro Pro Gln Asn Leu Gln Pro		
995	1000	1005
Glu Ser Asp Ala Pro Gln Gln Pro Gly Ser Ser Pro Arg Gly Lys Ser		
1010	1015	1020
Arg Ser Pro Ala Pro Pro Ala Asp Lys Glu Ala Phe Ala Ala Glu Ala		

1025		1030		1035		1040
Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro Phe						
	1045			1050		1055
Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro Asp						
	1060			1065		1070
Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu Gly						
	1075			1080		1085
Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile Ser						
	1090			1095		1100
Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu Glu						
1105		1110			1115	1120
Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His Val						
	1125			1130		1135
Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met Gly						
	1140			1145		1150
Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly Val						
	1155			1160		1165
Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser						
	1170			1175		1180
Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala						
1185		1190			1195	1200
Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr						
	1205			1210		1215
Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His						
	1220			1225		1230
Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile						
	1235			1240		1245
Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu						
	1250			1255		1260
Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser						
1265		1270			1275	1280
Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg						
	1285			1290		1295
Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr						
	1300			1305		1310
Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile						
	1315			1320		1325
Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His						
	1330			1335		1340
His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly Ile						
1345		1350			1355	1360
Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu Ala						
	1365			1370		1375
Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser Arg						
	1380			1385		1390
Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys Leu						
	1395			1400		1405
Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg						
	1410			1415		1420
Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu						
1425		1430			1435	1440
Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr						
	1445			1450		1455
Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His						

1460	1465	1470
Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val		
1475	1480	1485
His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys		
1490	1495	1500
Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly		
1505	1510	1515
Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys		
1525	1530	1535
Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala		
1540	1545	1550
Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro		
1555	1560	1565
Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg		
1570	1575	1580
Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr		
1585	1590	1595
Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu		
1605	1610	1615
Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala		
1620	1625	1630
Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala		
1635	1640	1645
Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His		
1650	1655	1660
Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu		
1665	1670	1675
Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met		
1685	1690	1695
His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg		
1700	1705	1710
Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly		
1715	1720	1725
Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu		
1730	1735	1740
Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala		
1745	1750	1755
Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser		
1765	1770	1775
Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr		
1780	1785	1790
Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp		
1795	1800	1805
Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu His		
1810	1815	1820
Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly		
1825	1830	1835
Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser		
1845	1850	1855
His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu		
1860	1865	1870
Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile		
1875	1880	1885
Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr		

1890	1895	1900
Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His Cys		
1905	1910	1915
Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu Pro		1920
	1925	1930
Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg Pro		1935
	1940	1945
Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg Ser		1950
	1955	1960
Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg Pro		1965
	1970	1975
Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro Ala		1980
1985	1990	1995
Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro Pro		2000
	2005	2010
Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro Phe		2015
	2020	2025
Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser Ser		2030
	2035	2040
Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro Ser		2045
	2050	2055
Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp Lys		2060
2065	2070	2075
Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val Lys		2080
	2085	2090
Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro Glu		2095
	2100	2105
Ser Gln Pro Ser Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val Lys		2110
	2115	2120
Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val Ile		2125
	2130	2135
Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro Leu		2140
2145	2150	2155
Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu Asp		2160
	2165	2170
Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His Gly		2175
	2180	2185
Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser Pro		2190
	2195	2200
Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Gly Glu Asp Gly Ile Glu		2205
	2210	2215
Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg Ser		2220
2225	2230	2235
Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro Ser		2240
	2245	2250
Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala Phe		2255
	2260	2265
Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys Lys		2270
	2275	2280
Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro Glu		2285
	2290	2295
Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala Ile		2300
2305	2310	2315
Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu His		2320

	2325		2330		2335
Ala	Ser	Thr	Asn	Met	Gly
	2340		2345		2350
Gly	Lys	Tyr	Asp	Gln	Trp
	2355		2360		2365
Phe	Asn	Pro	Leu	Asn	Ala
	2370		2375		2380
Thr	Ala	Ala	Asp	Gly	Arg
	2385		2390		2395
Gly	Gly	Lys	Ala	Lys	Val
	2405		2410		2415
Ser	Pro	Ala	Pro	Gly	Leu
	2420		2425		2430
Ser	Val	His	Ser	Glu	Gly
	2435		2440		2445
Arg	Val	Trp	Glu	Asp	Arg
	2450		2455		2460
Tyr	Asn	Pro	Leu	Ile	Met
	2465		2470		2475
Pro	Pro	Pro	Gly	Leu	Pro
	2485		2490		2495
His	Ala	Trp	Asp	Glu	Glu
	2500		2505		2510
Thr	Leu	Ser	Asp	Ser	Glu
	2515				

<210> 677

<211> 345

<212> DNA

<213> Homo sapiens

<400> 677

gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattgggtca gttcaccctt
60gagggtatag ctccggcacg ccgtgggtgtt ccacagattg aagttacttt cgatatcgat
120gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggtaagga acagaagatt
180cgcacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
240gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
300gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
345

<210> 678

<211> 110

<212> PRT

<213> Homo sapiens

<400> 678

Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly

1

5

10

15

Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

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<210> 679

<211> 362

<212> DNA

<213> Homo sapiens

<400> 679

```

acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

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<210> 680

<211> 100

<212> PRT

<213> Homo sapiens

<400> 680

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Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

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<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 681
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca
 60
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc
 120
 ggtttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aagggtgaaac gtgtgcttga gtagggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt
 357

<210> 682
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 682
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
 1 5 10 15
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 683
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
 60
 aatattgttt tgcccgcagc gtggttgcac gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca
 360
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5				10					15		
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
		20					25					30			
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35					40				45				
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50				55					60					
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65				70				75				80			
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90				95			
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
		100					105					110			
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120					125				
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
	130					135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aaccgcgaac gatggatgga ttgacactat tcggcctggt
 60
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct
 120
 gctgttcgcg gccgcttggc gctcgggttcg gcctacggct tcctccaagg cgcttgccg
 180
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
 240
 gcgatgaccg catcgtccgg cttaagcccg gaaacgaaac cgaccagtgc gctggtttga
 300
 tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
 1 5 10 15
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgac
 60
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt
 120
 ctcatgaaa cccacgggtg tgcacgatac gagcttcggg taccacctgc gtgcgcggtt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactgget tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```

      35      40      45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50      55      60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65      70      75      80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85      90      95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100      105      110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115      120      125
Phe Arg Asp Ile Phe Ala Asp Asp
      130      135

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<210> 689
 <211> 499
 <212> DNA
 <213> Homo sapiens

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<400> 689
cgcgctcgcg tactcgacgt cgattttcat caccgtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg caccggcgagc cggccgtgtc ctatccctac
120
tattcggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
240
aaactccagc aattctcgcc gcaggatttg gtgatctcac tgggggtcga caccttcaag
300
gacgaccgga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaagac ggcgtgata
499

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<210> 690
 <211> 157
 <212> PRT
 <213> Homo sapiens

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<400> 690
Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
1      5      10      15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20      25      30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35      40      45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50      55      60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691
 <211> 336
 <212> DNA
 <213> Homo sapiens

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<400> 691
ntgctgctg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggccccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgcccgacgc ctgctgcgca acggtgcct ttgctggct
180
ggaggcgcca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgctt gctgtggacc gccggc
336

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<210> 692
 <211> 112
 <212> PRT
 <213> Homo sapiens

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<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
100          105          110

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<210> 693
 <211> 580

<212> DNA

<213> Homo sapiens

<400> 693

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<211> 136

<212> PRT

<213> Homo sapiens

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20     25     30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35     40     45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50     55     60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65     70     75     80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85     90     95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100    105    110
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